

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2004, 01:08:10 ; Search time 5818 Seconds
(without alignments)
3585.934 Million cell updates/sec

Title: US-09-980-468-2

Perfect score: 2595

Sequence: 1 MALVDFLFLGTWTSKYSV.....AVVKALKEINDEASIRLUHAH 483

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2595	100.0	1467	6	AX058832 Sequence
2	2595	100.0	2040	6	AX058830 Sequence
3	2595	100.0	2040	8	CPU250734 Ceratodon
4	1619	62.4	2160	6	AX058840 Sequence
5	1619	62.4	2160	8	CPU250735 Ceratodon
6	1475	56.8	1578	6	AX481617 Sequence
7	1475	56.8	1578	6	AX481946 Sequence
8	1475	56.8	2012	6	AX069275 Sequence
9	1475	56.8	2012	8	PPAJ2980 Physcomit
10	1475	56.8	15430	6	AX481635 Sequence
11	1475	56.8	15430	6	AX481964 Sequence
12	1475	56.8	17752	6	AX481638 Sequence
13	1475	56.8	17752	6	AX481967 Sequence
14	1270	48.9	3518	8	PPAJ2981 Physcomit
15	925	35.6	520	6	AX058834 Sequence
16	852.5	32.9	1521	8	AB070555 Mortierel
17	841.5	32.4	1374	6	BD232180 Compositi
18	841.5	32.4	1617	6	AR080598 Sequence
19	841.5	32.4	1617	6	AR098439 Sequence
20	841.5	32.4	1617	6	AR136018 Sequence
21	841.5	32.4	1617	6	AR215236 Sequence
22	841.5	32.4	1617	6	AR235375 Sequence
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ALIGNMENTS

RESULT 1

AX058832
LOCUS AX058832 1467 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 3 from Patent WO0075341.
ACCESSION AX058832
VERSION AX058832.1 GI:12311152
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
REFERENCE 1
AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zehring, R.
TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 3 14-DEC-2000;
BASF AKTIENGESSELLSCHAFT (DE)
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ORIGIN
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Pred. No.: 2,28e-244 Length: 1467
Score: 2595.00 Matches: 483
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 41 AlaGlnGlyLysThrAlaGlyGlnThrLeuArgSerValGlnAspLysLysPro 60
DB 130 GGTCAAGGTAAACATCGCGGACAGACACTGAGACAGATCGGTGAGGACAAAAGCCA 189
QY 61 GlyThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCysTrpMetIle 80
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QY 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProProAla 120
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DB 850 GAAATTTTCGCCACCGCTTGGAGCAAGAAATTTCCGAGTGTCTCAATATCAGCACTAC 909
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DEFINITION
Sequence 1 from Patent WO0075341.
ACCESSION
AX058830
VERSION
AX058830.1
KEYWORDS
GI:12311150
SOURCE
Ceratonodon purpureus
ORGANISM
Ceratonodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
REFERENCE
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AUTHORS
Heinz, E., Symme, S., Lee, M., Girke, T., Sperling, P. and
Zaehring, U.
TITLE
g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL
Patent: WO 0075341-A 1 14-DEC-2000;
BASF AKTIENGESELLSCHAFT (DE)
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Alignment Scores:
Pred. No.: 3,49e-244 Length: 2040
Score: 2595.00 Matches: 483
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 QY 461 AlaSerValAlaValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeu 480
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RESULT 4
 AX058840
 LOCUS 2160 bp DNA linear PAT 17-JAN-2001
 DEFINITION Sequence 11 from Patent WO0075341.
 ACCESSION AX058840
 VERSION AX058840.1 GI:12311157

KEYWORDS Ceratodon purpureus
 SOURCE Ceratodon purpureus
 ORGANISM Ceratodon purpureus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

REFERENCE 1
 AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
 Zaehringer, U.
 TITLE g(d) 6-acetylase and g(d) 6-desaturase from ceratodon purpureus
 JOURNAL Patent: WO 0075341-A 11 14-DEC-2000;
 BASF AKT-ENGESSELLSCHAFT (DE)

FEATURES
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ORIGIN
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 Percent Similarity: 76.17% Conservative: 72
 Best Local Similarity: 51.51% Mismatches: 101
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 DB: 6 Gaps: 3

US-09-980-468-2 (1-483) x AX058840 (1-2160)

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QY 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
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RESULT 7
AX481946
LOCUS 1578 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 7 from Patent WO02057464.
ACCESSION AX481946
VERSION AX481946.1 GI:22316674
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
REFERENCE 1
AUTHORS Heinz, E., Duwenig, F., Bischoff, F., Drexler, H. and Lerchl, J. S.
TITLE Method for the expression of biosynthetic genes in plant seeds
JOURNAL using novel multiple expression constructs
Patent: WO 02057464-A 7 25-JUL-2002;
EAS PLANT SCIENCE GMBH (DE)

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Best Local Similarity: 55.31% Mismatches: 117
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RESULT 8

AX069275

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sequence 1 from Patent WO0102591.

AX069275

AX069275.1

GI:12579151

Physcomitrella patens

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DNA

linear

PAT 25-JAN-2001


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DEFINITION Sequence 25 from Patent WO02057465.
ACCESSION AX481635
VERSION AX481635.1 GI:22316538
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
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AUTHORS Domergue, P., Zaehring, U., Heinz, E., Renz, A. and Lerchl, J.
TITLE Method for producing polyunsaturated fatty acids, novel
biosynthesis genes and novel plant expression constructs
JOURNAL Patent: WO 02057465-A 25 25-JUL-2002;
BASF PLANT SCIENCE GMBH (DE)
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QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
Db 14798 GAGTATCTATGCTACCGGCACCTTGCAGAGTTTGAAGGCTTGAAGGATGTCGCG--- 14854
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Db 14855 GAGGCTCGCGAGGACGATGCT 14878

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PPAJ2981 3518 bp DNA linear PLN 23-OCT-1998

RESULT 14
PPAJ2981
LOCUS

DEFINITION Physcomitrella patens des6 gene.
ACCESSION AJ222981
VERSION 1.1 GI:3790208
KEYWORDS delta6-acyl-lipid desaturase; des6 gene.
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1
AUTHORS Girke,T., Schmidt,H., Zahringier,U., Reski,R. and Heinz,E.
TITLE Identification of a novel delta 6-acyl-group desaturase by targeted
gene disruption in Physcomitrella patens
JOURNAL Plant J. 15 (1), 39-48 (1998)
MEDLINE 98416756
PUBMED 9744093
REFERENCE 2 (bases 1 to 3518)
AUTHORS Girke,T.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik,
Universitaet Hamburg, Chhorststrasse 18, D-22609 Hamburg, GERMANY
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exon		145	AspTyrArgAspMetArgAlaGluPheValArgGluGlyLeuPheLysSerSerLysAla	164
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exon		165	TrpPheLeuGlnThrLeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIle	184
intron		2134	TACTATGTTATGCAAGCTGCTCAGCAATGTTGCTATTTTTCGCGAGCATTCGAATAATA	2193
exon		185	CysTyrAspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheVal	204
intron		2194	TGTTGAGCAAGACTATTTCAGCGGTTTGGCTTCAGCTTGATGATGCTCTGTGTGTTTC	2253
exon		205	GlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGln	217
intron		2254	CAACAGTCGGGATGCTATCCCATGATTTTCTCCCAATCAGGTTCGAAAAACCGTATTCA	2313
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exon		328	rThrLysGlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAl	348
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exon		348	aAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluSe	368
intron		2794	AGCGTGTCTCTCTCTCCCTGGT---TGAAGCCATTAGTATG3ATGGCGGTGACCTGAGT	2850
exon		368	uValAlaGlyLeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValry	388
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ORIGIN

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Percent Similarity:	46.58%	Conservative:	72
Best Local Similarity:	37.11%	Mismatches:	118
Query Match:	48.94%	Indels:	289
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US-09-980-468-2 (1-483) x PPAJ2981 (1-3518)

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Qy	38	LysValSer-----	40
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Qy	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer	54
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Qy	55	ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro	74
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Db	1534	AGGTTATACAGTAATCATGATGATGAACGGCGTTGCATGTTGAGTAATTCGACTCT	1593
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Db	1594	GTTATCCTGATTTGGCATTTGCTACGCCCGCTTCATCTGTTTGGATGNGGGGAAT	1653
Qy	85	-----ValTyrAspIleSerArgPheAla	92
Db	1654	TGCTGCCCTCAATTAAGGTATTGTTTAATCACAGGTTGATGATTTTCCAAATTTTGG	1713
Qy	93	AspAspHisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspVal	112
Db	1714	GACGAGCATCCCGAGGATCAGTTATTAGTATTATTGTCAGCAGAGCGGACAGATGTT	1773
Qy	113	PheAlaThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyVasp	132
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D 3030 GGTGGGGCCCTTTGAGATAGAGATAGATAGTACCTCCAAATCTTTCTTAAATAAGT 3089
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QY 403 gAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleG 423
D 3210 GGATATCAAGGAAGCAATATTCACAGCACTGTTTCACTGTGTGGCTTAAACAGGCAATAGA 3269
QY 423 uHisHisLeuPheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValG 443
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D 3330 GGTGTTCTGTAAAGAACACCGTCTGGTGTACGAAGACGTATCTATTCTCCGGCACTTG 3389
QY 463 lAlaValValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeuHisAla 482
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RESULT 15

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AX058834 LOCUS 520 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 5 from Patent WO0075341.
ACCESSION AX058834
VERSION AX058834.1 GI:12311154
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
REFERENCE 1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zachringer, U.
TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 5 14-DEC-2000;
BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
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ORIGIN

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Score: 925.00 Matches: 172
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.42% Mismatches: 0
Query Match: 35.65% Indels: 0
DB: 6 Gaps: 0

US-09-980-468-2 (1-483) x AX058834 (1-520)
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QY 291 IleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArg 310
D 122 ATTTTGGAGTGTCTTCGATATCAGACTACATGATTCGCTCTATTGTTTCATGGCCCGG 181
QY 311 TyrSerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLys 330
D 182 TACAGTTGGACTTTTGGAGTTTCTCTTCACATTCATCTGATTTGAGCAACCAAG 241
QY 331 GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPhe 350
D 242 GGATTGATAGAGAAAGGAAACAGTTGCTTTTCACTACGCTGCTTTCAGTTGGGCTGCGTTC 301
QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370
D 302 CATATTTTGGCGGTGTCGCTAACCTCTTCGCTGGATGGTAGCACTGAGCTTGTGGCC 361
QY 371 GlyLeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu 390
D 362 GGTTCGTTTGGGATTGCTGTTTACGTTGAGTCACAATGGAAGAGGTTTACAATGAA 421
QY 391 SerLysAspPheValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPhe 410
D 422 TCGAAGGACTTCGTGAGAGCCCGAGTTATTACCACCCCGTAACACCAAGCGAGGTGCTTC 481
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D 482 AACGATTGGTTCACTGGGAGACTCCACACCCAGATTGAG 520

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Search completed: June 19, 2004, 04:44:23

Job time : 5938 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 20:19:04 ; Search time 7900 Seconds
(without alignments)
11192.378 Million cell updates/sec

Title: US-09-980-468-1

Perfect score: 2040

Sequence: 1 ctcaggcaggtctcagttga.....aaaaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

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16: em.fun.*

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41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2040	100.0	2040	8	CPU250734 Ceratodon
3	1456.4	71.4	1467	6	AX058832 Sequence
4	670	32.8	2160	6	AX058840 Sequence
5	670	32.8	2160	8	CPU250735 Ceratodon
6	567.4	27.8	1578	6	AX481617 Sequence
7	567.4	27.8	1578	6	AX481946 Sequence
8	567.4	27.8	2012	6	AX069275 Sequence
9	567.4	27.8	2012	8	PPAJ2980 Physcomit
10	567.4	27.8	15430	6	AX481635 Sequence
11	567.4	27.8	15430	6	AX481964 Sequence
12	567.4	27.8	17752	6	AX481638 Sequence
13	567.4	27.8	17752	6	AX481967 Sequence
14	518.4	25.4	520	6	AX058834 Sequence
15	254.6	12.5	514	6	AX058836 Sequence
16	244.2	12.0	3518	8	PPAJ2981 Physcomit
17	153	7.5	1617	6	ARC05098 Sequence
18	153	7.5	1617	6	ARC08439 Sequence
19	153	7.5	1617	6	ARI36018 Sequence
20	153	7.5	1617	6	AR215236 Sequence
21	153	7.5	1617	6	AR235375 Sequence
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23	153	7.5	1617	6	BD092914 Methods a
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27	145	7.1	1374	8	AF306634 Mortierel
28	144.8	7.1	1590	8	AB020032 Mortierel
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33	136.4	6.7	1521	8	AB070555 Mortierel
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36	111.4	5.5	2207	8	AB070557 Mortierel
37	100.8	4.9	1743	8	AB070556 Mortierel
38	99.8	4.9	1947	8	AF465283 Mortierel
39	99.4	4.9	1341	8	AF536525 Anemone 1
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41	96	4.7	560	6	BD147335 Primer fo
42	96	4.7	1335	6	AX253298 Sequence
43	96	4.7	1686	6	AR221958 Sequence
44	96	4.7	1686	6	BD082638 Methods a
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ALIGNMENTS

RESULT 1
AX058830 2040 bp DNA Linear PAT 17-JAN-2001
LOCUS Sequence 1 from Patent WO0075341.
DEFINITION AX058830
ACCESSION AX058830.1 GI:12311150
VERSION AX058830.1
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
Bkaryota; Viridiplantae; Streptophyta; Bryophyta;
Bryopsida; Dicranales; Dicranaceae; Ceratodon.
REFERENCE 1
AUTHORS Heinz E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zaehring, U.
TITLE _g(d)6-acetylenase and _g(d)6-desaturase from ceratodon purpureus

Pred. No. is the number of results predicted by chance to have a


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Qy 1501 TTTTGATGCAACAGTAGTACATTCATTAAGACATATGTCGAGATATAATTGCGAGTGT 1860
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Db 1861 TCTATTGAGCGGGGATAGTACTAGTCCATATCGCGGTTGCGGAGTATTACATTATTA 1920
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Db 1921 GTTGCCACAAAGTAGATCTAGTGTAAATTTCTATTTCGCCATGTAATATTACTCTCAA 1980
Qy 1981 TATATACGGTTATCTATTCTTCTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 TATATACGGTTATCTATTCTTCTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 2
CPU250734 2040 bp mRNA linear PLN 21-JUN-2000
DEFINITION Ceratodon purpureus mRNA for delta 6-fatty acid acetylase.
ACCESSION AJ250734
VERSION AJ250734.1 GI:8670976
KEYWORDS acetylase; cytochrome b5; delta 6-fatty acid acetylase.
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
REFERENCE 1
AUTHORS Sperling, P., Lee, M., Girke, T., Zahring, U., Stymne, S. and Heinz, E.
TITLE A bifunctional delta-fatty acyl acetylase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily
JOURNAL Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE 20307617
PUBMED 10848999
REFERENCE 2 (bases 1 to 2040)
AUTHORS Sperling, P.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology, Institut fuer Allgemeine Botanik, Universitaet Hamburg, Chloerstrasse 18, D-22609 Hamburg, GERMANY

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176. .1627
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1628. .2003
3'UTR
ORIGIN

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Db 61 CGGCACCTTGTGGATGTGTGAAGGAGTGATCGATCAGGAGTGCAGGAGCTGCAATTAGTTTC 120
Qy 121 TCAGGTCGATCAGCGTTATCTGAAAAAGGCTGCGTCTGTGAGCAGTGTGCAAAATGCG 180
Db 121 TCAGGTCGATCAGCGTTATCTGAAAAAGGCTGCGTCTGTGAGCAGTGTGCAAAATGCG 180
Qy 181 CCTCGTTACCGACTTCTGAACTTCTCGGACAGCATGAGCAAGTGCAGCGTGTACAC 240
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RESULT 3

AX058832

LOCUS

DEFINITION Sequence 3 from Patent WO0075341.

AX058832 1467 bp DNA linear PAT 17-JAN-2001

ACCESSION

AX058832.1 GI:12311152

VERSION

AX058832.1

KEYWORDS

Ceratonodon purpureus

SOURCE

Ceratonodon purpureus

ORGANISM

Ceratonodon purpureus

REFERENCE

Heinz, E., Symne, S., Lee, X., Girke, T., Sperling, P. and Zaehring, U.

AUTHORS

g(d)6-acetylase and g(d)6-desaturase from ceratonodon purpureus

TITLE

Patent: WO 0075341-A 3 14-DEC-2000;

JOURNAL

BASP AKIENGESBILLSCHAFT (DE)

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Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity

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99.9%; Pred. No. 0;

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AX058840
LOCUS AX058840 2160 bp linear PAT 17-JAN-2001
DEFINITION Sequence 11 from Patent WO0075341.
ACCESSION AX058840
VERSION AX058840.1 GI:12311157

KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
REFERENCE 1
AUTHORS Heinz, B., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zaehrer, U.
TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 11 14-DEC-2000;
BASF AKT-ENGESSELLSCHAFT (DE)
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ORIGIN

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ACCESSION AJ250735
VERSION AJ250735.1 GI:8670978
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SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
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AUTHORS Sperling, P., Lee, M., Girke, T., Zahrlinger, U., Stymne, S. and Heinz, B.
TITLE A bifunctional delta-fatty acyl acyltransferase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily
JOURNAL Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE 20307617
PUBMED 10848999
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REFERENCE

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2 (bases 1 to 2160)
Sperling, P.
Direct Submission
Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology,
Institut fuer Allgemeine Botanik, Universitaet Hamburg,
Ohnhorststrasse 18, D-22609 Hamburg, GERMANY
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RESULT 6
AX481617
LOCUS 1578 bp DNA linear 2AT 16-AUG-2002
DEFINITION Sequence 7 from Patent WO02057465.
ACCESSION AX481617
VERSION AX481617.1 GI:22316520
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1
Domergue, F., Zaehring, U., Heinz, E., Reiz, A. and Lersch, J.
METHOD for producing polyunsaturated fatty acids, novel
biosynthesis genes and novel plant expression constructs
Patent: WO 02057465-A 7 25-JUL-2002;
JOURNAL

FEATURES
source BASF PLANT SCIENCE GMBH (DE)
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ORIGIN
Query Match 27.8%; Score 567.4; DB 6; Length 1578;
Best local Similarity 66.3%; Pred. No. 2.5e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
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RESULT 7
AX481946 LOCUS 1578 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 7 from Patent WO202057464.
ACCESSION AX481946
VERSION AX481946.1 GI:22316674
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens

REFERENCE 1
AUTHORS Heinz, B., Duwenig, E., Bischoff, F., Drexler, H. and Lerchl, J. S.
TITLE Method for the expression of biosynthetic genes in plant seeds
using novel multiple expression constructs
JOURNAL Patent: WO 02057464-A 7 25-JUL-2002;
BAS: PLANT SCIENCE GMBH (DE)
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ORIGIN

Query Match 27.8%; Score 567.4; DB 6; Length 1578;
Best Local Similarity 66.3%; Pred. No. 2.5e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
QY 359 ACTTACTCTCTGGCGCGATGTGCTTCTCACACAGGCTTGAGACTGCTGTGATGATCGTC 418
Db 310 ACACACCCCTTATCAGAAGTAGCAGTACACAAAGCCAGGATGCTGCGATGTTCTGA 369
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QY 779 CTCTTCGTCACACAGTGTGGATGGCTTCCCATGATTTTCCITCATCAACAGCTTTTCAG 838
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DEFINITION Sequence 1 from Patent WO0102591.
ACCESSION AX069275
VERSION    AX069275.1      GI:12579151
KEYWORDS   Physcomitrella patens
SOURCE     Physcomitrella patens
ORGANISM   Physcomitrella patens
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Funariaceae; Funariales; Physcomitrella.

REFERENCE
  1. Heinz, E., Girke, T., Scheffler, J. and da Costa e Silva, O.
    Plants expressing g(d)6-desaturase genes and oils from these
    plants containing pufas and method for producing unsaturated fatty
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    JOURNAL Patent: WO 0102591-A 1 11-JAN-2001;
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ORIGIN
Query Match      27.8%; Score 587.4; DB 6; Length 2012;
Best Local Similarity 66.3%; Pred. No. 2.7e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY      359 ACTTACTCTCTGGCGGATGTTGCTTCTCAACGACGCGCTCGGACTGCTGGATGATGCTC 418
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Db 1825 ACTTGCAAGGTTTGAAGCAATGAAGGAAGTCCGGAGGCTCGCGCAGAGCAGCAT 1881

RESULT 9

PPAJ2980 2012 bp mRNA linear PLN 23-OCT-1998

LOCUS Physcomitrella patens mRNA for delta6-acyl-lipid desaturase.

DEFINITION AJ222980

ACCESSION AJ222980.1 GI:3790206

VERSION delta6-acyl-lipid desaturase; des6 gene.

KEYWORDS Physcomitrella patens

SOURCE Physcomitrella patens

ORGANISM Bryopsida; Funariidae; Funariaceae; Bryophyta; Physcomitrella.

REFERENCE 1

AUTHORS Girke, T., Schmidt, H., Zahring, U., Reiki, R. and Heinz, E.

TITLE Identification of a novel delta 6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens

JOURNAL Plant J. 15 (1), 39-48 (1998)

MEDLINE 98416756

PUBMED 9744093

REFERENCE 2 (bases 1 to 2012)

AUTHORS Girke, T.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik, Universitaet Hamburg, Ohthorststrasse 18, D-22609 Hamburg, GERMANY

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 27.8%; Score 567.4; DB 8; Length 2012;

Best Local Similarity 66.3%; Pred. No. 2.7e-145;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGCCCGATGTTGCTTCTCAGCAGCGCTCGGACTGCTGGATGATCGTC 418

Db 628 ACACACCCCTTATCAGAGTAGCAGTACACACAGCAGGATGCTGGATTGTTSTA 687

QY 419 AAAGAGAGGTGTATGATATTAGCCGTTTTCGGAGCAGCACCCCTCGAGGAGCGTAAAT 478

Db 688 AAAAAAAGGTTGATGATGTTTCCAAATTTTCGGAGCAGCATCCCGAGGATCAGTTAT 747

QY 479 AGCACCTACTTTCGGCGGGATGGCACAGAGTTTTCGCAACATTCATCCACCTCCCGCA 538

Db 748 AGTACTTTATTTTGGAGAGACGCGCACAGATGTTTCTCTAGTTTTCATGCAGCTTCTACA 807

QY 539 TGAAGCAACATCATGACTACTACTACATTTGGAGACCTTCTGTAGGAGAGGCCCTTGTAGAA 598

Db 808 TGAAGAAATCTTCAAGACTTTTACATTTGGTGTGAGTGGAGGGTGGAGCCGACTCCAGAG 867

QY 599 TTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTGTAGAGAGGGCTTTTCAAGAGT 658

Db 868 CTGCTGAAGATTTCCGAGAAATGAGAGCTCTTTTCTGTAGGAGGACAACTTTTCAAGAGT 927

QY 659 TCCAAAGCCCTGGTTCCTGCTTCAGACTCTGATTAATGACAGCTCTCTTTTGTGTGAGAGT 718

Db 928 TCGAAATTTGACTATGTTATGAAGCTGCTCACGAATGTTGCTATTTTGTGTGCGAGCAT 987

QY 719 GCGACTATCTGTTACGACAGAGTTACTGGGCTATTGCTGTGCTGTGACAGCTTTGATGGGT 778

Db 988 GCAATAATATGTTGGAGCAAGCTATTTCAGCGGTTTGGCTTCAGCTTGTATGATGGCT 1047

QY 779 CTCTTCGTCCAAACAGTGTGATGGCTTGCCTCATGATTTCTTTCATCAACAGCTCTTTTTCAG 838

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QY 959 CAGTACACACCTCTAGACGAGACATTTGATCTCTCCCATCATTCCTCGGAGCAAGGAA 1018

Db 1228 ACTTACCAACCAATTTGATGAAGATATTGATCTCTCCCTCATTCCTGCTGGAGCAAGGAC 1287

QY 1019 ATTTTGGCCACCGTTGAGAGCAGAGAAATTTTGGAGTGTCTCAATATCAGCATCATG 1078

Db 1288 ATACTGCCACAGTTGAGAAATAGACATTTCTCGAATCTCTCAATACCAAGCACTCTGTC 1347

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Db 1348 TTCTATGGTCTGTATTTTTCGCCCGTGTGATTTGCTCTTTTGGAGTGGAGATATACC 1407

QY 1139 TTCAATTCCTGATTTGAGACGACCAAGAGATGATAGAGAGGAAACAGTTGCTTTTTCAC 1198

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Db 1645 ACACGGGATATCAAGAGAAACATTTTCAACGACTGGTTTCACTGGTGGCTTTAAACAGCAA 1704

QY 1439 ATTGAGCATCACTGTTTTCAAACATTCGCCAGGCAACAATACCCCAAGATTCGACCTCAG 1498

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QY 1499 GTGAGGCTCTTTTGAAGAGCAGGCTTCGAGTAGGATGATGTTCTCCGTCGTTGTTGCC 1558

Db 1765 GTGGAGGTGTTCTGTGAAGAAACACGCTGTTGTTGTACGAAGAGCTATCTATTGTACCGGC 1824

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Db 14759 GTGAGGCTCTCTGTAAGAACACGGCTGCTGTGTACGAGACGCTATCTATTGCTACCGC 14818

Qy 1559 TCTGTCGGGTGTGAGGCGCTCAAGAAATGCTGATGAGCGTCAATTCGGCTT 1615
Db 14819 ACTTGCAAGGTTTGAAGACATTAAGAGATGCGGAGGCTGCGGAGACGACAT 14875

RESULT 13

AX481967
LOCUS AX481967 17752 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 28 from Patent WO02057464.
ACCESSION AX481967
VERSION AX481967.1 GI:22316695

KEYWORDS unidentified
SOURCE unclassified.

ORGANISM

Heinz, E., Duwenig, E., Bischoff, F., Drexler, H. and Lerchl, J.S.

AUTHORS Method for the expression of biosynthetic genes in plant seeds

TITLE using novel multiple expression constructs

JOURNAL Patent: WO 02057464-A 28 JUL-2002;

Basf Plant Science GmbH (DE)

FEATURES

1. 17752

Location/Qualifiers

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/db_xref="taxon:32644"

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Promotor-Terminator- Expressionsskassetten inseriert mit

Physcomitrella Elongase + Desaturase + Phaeodactylum

Desaturase"

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VYHSSISLWALAHAPGGEAYMSAALNSGVHVMYAYIFLAACLRSPKKNYL

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ORIGIN

Query Match 27.8%; Score 567.4; DB 6; Length 17752;
Best Local Similarity 66.3%; Pred. No. 4.5e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

Qy 359 ACTTACTCTCTGGCCGATGTGCTTCTCAGACAGGCGCTCGAGACTCTGATGATGCTC 418
Db 13622 ACACCCCCCTTTCAGAGTAGCAGTACACACAGCCAGCGATGCTGATGTTGTA 13682
Qy 419 AAGAGAGAGTGTATGATATTTAGCCGTTTTCGCGACGACCCCTCGAGGAGCGTAAT 478
Db 13682 AAAAAAAGGTGTATGATGTTTCCAAATTTTCGCGACGAGCATCCCGAGGATCAGTTAT 13741
Qy 479 AGCACTTACTTGGCGCGGATGGCAGACAGCTTTCGCAACATTCATCCACCTGCCGCA 538
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Qy 599 TTGCTTAAAGACTACAGATATCAGAGCCGAGTTTGTAGAGAGGGCTTTTCAAGAGT 658
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Db 14102 AACGCTCCGCTTAAAGTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT 14161
Qy 899 GTATCATGTTGGAGAGAGAGCAACATTCATCATCTCTCGGATGAGTGGGACGAA 958
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Db 14819 ACTTGAAGTTTGAAGCACTTGAAGGAGTCCGGAGGCTCGGAGACAGCAT 14875

RESULT 14
AX058834
LOCUS 520 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 5 from Patent WO0075341.
ACCESSION AX058834
VERSION AX058834.1 GI:12311154
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
REFERENCE 1
AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehring, U.
TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
FEATURES
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ORIGIN
Query Match 25.4%; Score 518.4; DB 6; Length 520;
Best Local Similarity 99.8%; Pred. No. 7e-132;
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CATTCATCATCTGCTCCGAATGAGTCGACGACAGTACACCTCTAGACGAGACAT 984
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QY 985 TGATCTCTCCCATCATCTGCTCCGAATGAGTCGACGACAGTACACCTCTAGACGAGACAT 1044
Db 61 TGATCTCTCCCATCATCTGCTCCGAATGAGTCGACGACAGTACACCTCTAGACGAGACAT 120
QY 1045 AATTTTCGAGTGTCTCAATATCAGACTACATGATTCGCTCTATTGTTTCATGGCCCG 1104
Db 121 CATGTTGCGAGTCTTTCAGTACGACGACCTATTCTTTTGGTTCTTTGAGCTTTGCGCG 180
QY 1105 GTACAGTTGAGCTTTTGGAGCTTTGCTCTTCAATTCATCTGATTTGAGCAGACAA 1164
Db 181 GTACAGTTGAGCTTTTGGAGCTTTGCTCTTCAATTCATCTGATTTGAGCAGACAA 240
QY 1045 AATTTTCGAGTGTCTCAATATCAGACTACATGATTCGCTCTATTGTTTCATGGCCCG 1104
Db 121 CATGTTGCGAGTCTTTCAGTACGACGACCTATTCTTTTGGTTCTTTGAGCTTTGCGCG 180
QY 1165 GGGATTGATAGAGGGAACAGTTGCTTTTCACTAGCCCTGTTTCAGTTGGGCTGGTT 1224
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Db 481 CAACGATTTGTTTCACTGGGGAGCTCGACACCCAGATTGAG 520

RESULT 15
AX058836
LOCUS 514 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 7 from Patent WO0075341.
ACCESSION AX058836
VERSION AX058836.1 GI:12311155
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
REFERENCE 1
AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehring, U.
TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 7 14-DEC-2000;
BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
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ORIGIN
Query Match 12.5%; Score 254.6; DB 6; Length 514;
Best Local Similarity 69.6%; Pred. No. 7.2e-59;
Matches 360; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 925 CATTCATCATCTGCTCCGAATGAGTCGACGACAGTACACCTCTAGACGAGACAT 984
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QY 1225 CCATATTTTGCCTGGTGTGCTTAAGCCTCTTTCGCTGATGTTAGCACTGAGCTTTGTGC 1284
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QY 1345 ATCGAAGGACTTCGTGAGAGCCGAGGTTATTACCCGTTACACCAAGCGAGGCTGGTT 1404
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 QY 418 GTCAAAGGACTTCGTGAATGCCAGATTGCATCGACTCCGACATCAAAAGCAGGGGTGT 477
 Db |||||
 QY 1405 CAACGATTGGTTCACTGGGGGACTCGACACCCAGATT 1441
 Db |||||
 QY 478 TATGATTGGTTACCGGAGGTCTCACACAGAGATT 514
 Db |||||

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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	670	32.8	2160	AAF25734	Aaf25734 C. purpur
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5	567.4	27.8	1578	ABQ76782	Abq76782 P. patens
6	567.4	27.8	2012	AAF26040	Aaf26040 P. patens
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11	567.4	27.8	17752	ABQ76797	Abq76797 pBARAI en
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13	254.6	12.5	514	AAF25732	Aaf25732 C. purpur
14	153	7.5	1617	AAF63624	Aaf63624 cDNA enco
15	153	7.5	1617	AAO0889	Aao0889 Mortierel
16	153	7.5	1617	AAA09430	Aaa09430 M. alpina
17	152.2	7.5	1374	AAF25234	Aaf25234 Nucleotid
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19	137.6	6.7	451	AAH56929	Aah56929 P patens
20	137.6	6.7	451	AAH56909	Aah56909 P patens
21	137.6	6.7	451	AAH50922	Aah50922 Lipid mod
22	114	5.6	1380	6 AAD35090	Aad35090 Pythium i
23	103.4	5.1	1471	3 AAD01349	Aad01349 Florida b

24	96	4.7	560	4	AAH05343	Aah05343 Human cDN
25	96	4.7	1335	4	AAAD19403	Aad19403 Human del
26	96	4.7	1474	3	AAF21845	Aaf21845 Human bre
27	96	4.7	1575	6	ABL90108	Ab190108 Human pol
28	96	4.7	1686	2	AAV63641	Aav63641 Contig 25
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31	96	4.7	1686	3	AAA14592	Aaa14592 Nucleotid
32	96	4.7	1686	3	AAA09451	Aaa09451 Human con
33	96	4.7	1686	3	AAA49337	Aaa49337 Human del
34	96	4.7	1686	6	ABS76711	Ab576711 Human des
35	96	4.7	1686	6	ABS71824	Ab571824 Human del
36	96	4.7	1843	2	AAV63642	Aav63642 Contig 25
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38	96	4.7	1843	2	AAV82641	Aav82641 Contig 25
39	96	4.7	1843	3	AAA14593	Aaa14593 Nucleotid
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42	96	4.7	1843	6	ABS76712	Ab576712 Human des
43	96	4.7	1843	6	ABS71825	Ab571825 Human del
44	96	4.7	2146	4	AAH15815	Aah15815 Human cDN
45	96	4.7	2190	4	AAH16118	Aah16118 Human cDN

ALIGNMENTS

RESULT 1
AAF25729 AAF25729 standard; DNA; 2040 BP.
XX
AC AAF25729;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
XX
OS Ceratodon purpureus.
XX
FH Key Location/Qualifiers
FT CDS 176..1627
FT /*tag= a
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PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.
XX
FA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX
DR WPI; 2001-112150/12.
DR P-ESDS; AAB46435.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX producing plant oils with increased content of unsaturated fatty acids.
PS Claim 1a; Page 41-44; 69pp; German.
XX
CC This invention describes a novel isolated nucleic acid (I) encoding
XX polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or

CC more regulatory sequences; (c) a vector containing (I) and EC; (d) CC organisms containing (I), EC or the vectors of (c); (e) preparation of CC unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by CC method (g). (I) are used to produce transgenic plants (or other CC organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by CC homology screening. (A), or TG containing them, are useful in human CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can CC be used to suppress expression of (III), resulting in oils with increased CC content of saturated fatty acids

XX Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Fred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCAGGCGAGTCTCAGTTCATGAGAGCGTCAAGTCTTGAATCCCTTTCAGGCTGTCTCAGGCT	60
DB	1	CTCAGGCGAGTCTCAGTTCATGAGAGCGTCAAGTCTTGAATCCCTTTCAGGCTGTCTCAGGCT	60
QY	61	CGGCACTTGTGGATGGTGAAGAGTGTTCGATCAGGAGTGCAGGAGTGCATTAGTTTC	120
DB	61	CGGCACTTGTGGATGGTGAAGAGTGTTCGATCAGGAGTGCAGGAGTGCATTAGTTTC	120
QY	121	TCAGGTCGATCAGGTTATTCTGAAAGAGTCCGCTCTGTGAGCAGTTTGCRAAAATGGC	180
DB	121	TCAGGTCGATCAGGTTATTCTGAAAGAGTCCGCTCTGTGAGCAGTTTGCRAAAATGGC	180
QY	181	CCTCGTTACCGACTTCTGAACTTTCTGGCAGCAGCATGAGCAAGTGCAGCGTGTACAC	240
DB	181	CCTCGTTACCGACTTCTGAACTTTCTGGCAGCAGCATGAGCAAGTGCAGCGTGTACAC	240
QY	241	CCATAGCTATCTGGAATCATGGGCTACTTTGAAGCAGCCCAAAAGTTTCTGCTCA	300
DB	241	CCATAGCTATCTGGAATCATGGGCTACTTTGAAGCAGCCCAAAAGTTTCTGCTCA	300
QY	301	AGTAAACTCGGGGACAGACACTGAGACAGAGTCCGTGACGACAAAGCCAGGCAC	360
DB	301	AGTAAACTCGGGGACAGACACTGAGACAGAGTCCGTGACGACAAAGCCAGGCAC	360
QY	361	TTACTCTCTGGCCGATSTTCTCTCACGACAGGCTGGAGACTGCTGATGATCGTCAA	420
DB	361	TTACTCTCTGGCCGATSTTCTCTCACGACAGGCTGGAGACTGCTGATGATCGTCAA	420
QY	421	AGAGAGGTGTATGATATTAGCGGTTTGGGACGACCCCTGGAGGAGCGGTAAATTAG	480
DB	421	AGAGAGGTGTATGATATTAGCGGTTTGGGACGACCCCTGGAGGAGCGGTAAATTAG	480
QY	481	CACCTACTTTGGGCGGATGGACAGACCTTTTCGCAACATTCATCCACCTGCCGCATG	540
DB	481	CACCTACTTTGGGCGGATGGACAGACCTTTTCGCAACATTCATCCACCTGCCGCATG	540
QY	541	GAAGCAACTCAATGACTACTACATTTGAGAGCTTGTAGGAGAGCCCTTGTATGAAAT	600
DB	541	GAAGCAACTCAATGACTACTACATTTGAGAGCTTGTAGGAGAGCCCTTGTATGAAAT	600
QY	601	GCTTAAAGACTACAGAGATGAGGCGGTTTGTAGAGAGGCTTTTCAAGAGTTTC	660
DB	601	GCTTAAAGACTACAGAGATGAGGCGGTTTGTAGAGAGGCTTTTCAAGAGTTTC	660
QY	661	CAAGGCTCGGTTCTGCTTCTGAGTCTGATTAATGAGCTCTCTTTGCTGGAGATTGC	720
DB	661	CAAGGCTCGGTTCTGCTTCTGAGTCTGATTAATGAGCTCTCTTTGCTGGAGATTGC	720
QY	721	GACTATCTGTTACGACAGAGTTACTGGGCTATTGTGCTGTACGCCAGTTTGTATGAGGCT	780
DB	721	GACTATCTGTTACGACAGAGTTACTGGGCTATTGTGCTGTACGCCAGTTTGTATGAGGCT	780

QY	781	CTTCGTCCAAACAGTGTGGATGGCTTGCCTCCCAAGATTTCTCTCATCAACAGGCTCTTGAGAA	840
DB	781	CTTCGTCCAAACAGTGTGGATGGCTTGCCTCCCAAGATTTCTCTCATCAACAGGCTCTTGAGAA	840
QY	841	CGGTACCGGGAACCTCTCTTTTGGCTATTGTTTGGCAATTTGGTGTCTTGGCTTTAGTGT	900
DB	841	CGGTACCGGGAACCTCTCTTTTGGCTATTGTTTGGCAATTTGGTGTCTTGGCTTTAGTGT	900
QY	901	ATCATGCTGGAGGACCAAGACCAACATTCATCATCTACTGCTCCGAATGAGTGGCAAGACA	960
DB	901	ATCATGCTGGAGGACCAAGACCAACATTCATCATCTACTGCTCCGAATGAGTGGCAAGACA	960
QY	961	GTCACACCTCTAGAGAGAGACATTTGATCTCTCCCATCATTTGCCCTGGAGCAAGGAAT	1020
DB	961	GTCACACCTCTAGAGAGAGACATTTGATCTCTCCCATCATTTGCCCTGGAGCAAGGAAT	1020
QY	1021	TTTGGCCACCGTTGAGAGCAAGAGAAATTTTGGAGTGTCTCAATATCAGCACTACATGAT	1080
DB	1021	TTTGGCCACCGTTGAGAGCAAGAGAAATTTTGGAGTGTCTCAATATCAGCACTACATGAT	1080
QY	1081	TCCTGCTCTATTGTTTCATGCGCCGGTACAGTTGCACTTTTGGAAAGTTTGGCTCTTCACAT	1140
DB	1081	TCCTGCTCTATTGTTTCATGCGCCGGTACAGTTGCACTTTTGGAAAGTTTGGCTCTTCACAT	1140
QY	1141	CAATCCTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGGAACAGTTTCTTTCCTACTA	1200
DB	1141	CAATCCTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGGAACAGTTTCTTTCCTACTA	1200
QY	1201	CGCTCGTTTCACTGCTGCTGCTTCCATATTTTCCCGGGTGTGCTTAAGCTCTCTGCGTG	1260
DB	1201	CGCTCGTTTCACTGCTGCTGCTTCCATATTTTCCCGGGTGTGCTTAAGCTCTCTGCGTG	1260
QY	1261	GATGTAGCAACTGAGCTTGTGCGGTTTGTGTTGGGATTCGTGTTTACGTTTACGTTGATCA	1320
DB	1261	GATGTAGCAACTGAGCTTGTGCGGTTTGTGTTGGGATTCGTGTTTACGTTTACGTTGATCA	1320
QY	1321	CAATGAAAGGAGGTTTACAAATCGAAGGACTTCTGAGAGCCAGGTATATACAC	1380
DB	1321	CAATGAAAGGAGGTTTACAAATCGAAGGACTTCTGAGAGCCAGGTATATACAC	1380
QY	1381	CGCTAACCAACAGCGAGGCTGTTTCAACGATTTGTTTCACTGGGGGACTCGACACCCAGAT	1440
DB	1381	CGCTAACCAACAGCGAGGCTGTTTCAACGATTTGTTTCACTGGGGGACTCGACACCCAGAT	1440
QY	1441	TGAGCATACCTGTTTCCAAATGAGGCTGAGTCCCACTCCCAAGATCCCACTCAGGT	1500
DB	1441	TGAGCATACCTGTTTCCAAATGAGGCTGAGTCCCACTCCCAAGATCCCACTCAGGT	1500
QY	1501	CGAGGCTCTTTGCAAGAGCAGCGGCTCGAGTACGATATGTTCTCGTCTGTTGGTGCCTC	1560
DB	1501	CGAGGCTCTTTGCAAGAGCAGCGGCTCGAGTACGATATGTTCTCGTCTGTTGGTGCCTC	1560
QY	1561	TGTTCGGGTTGTGAAGGCGCTCAAGGAAATTTGATGAAGCGTCAATTCGGCTTCAAGC	1620
DB	1561	TGTTCGGGTTGTGAAGGCGCTCAAGGAAATTTGATGAAGCGTCAATTCGGCTTCAAGC	1620
QY	1621	TGACTTAAGAAATCGTGAAGTGTGACTTATTTTTCGCTGCTGCTCAATTTGTT	1680
DB	1621	TGACTTAAGAAATCGTGAAGTGTGACTTATTTTTCGCTGCTGCTCAATTTGTT	1680
QY	1681	CGGGAGCAGGCTTGGCAGTGTGTTTCAACCGGAGGCGACTGAAAATGTGAGAAATCCAT	1740
DB	1681	CGGGAGCAGGCTTGGCAGTGTGTTTCAACCGGAGGCGACTGAAAATGTGAGAAATCCAT	1740
QY	1741	TTCGAGAAATACCAATTCCTAGCTAAATCTTCTTTTACAGTCCGATATATGAAACTT	1800
DB	1741	TTCGAGAAATACCAATTCCTAGCTAAATCTTCTTTTACAGTCCGATATATGAAACTT	1800
QY	1801	TTTGTGATCAACAGTAGTACATTCATTTGAAGACATTTTTCGAGATATATTCAGTGT	1860
DB	1801	TTTGTGATCAACAGTAGTACATTCATTTGAAGACATTTTTCGAGATATATTCAGTGT	1860
QY	1861	TCTATTTCAGCGGCGATACGTTACTAGTCCATATCGGCGGTTTTCGAGAGTTTACATTATTA	1920

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Db 1861 TCTATTGAGCGGCTACGACTAGTCCATATCGCGGTTGCGGAGTTTACATATTA 1920
QY 1921 GTGGCACAACGAGTAGATAGTCTAATTTCTATTTCCGATCATTAATATTACTGAA 1980
Db 1921 GTGGCACAACGAGTAGATAGTCTAATTTCTAATTTCCGATCATTAATATTACTGAA 1980
QY 1981 TATATACCGTATCTATTTCTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 TATATACCGTATCTATTTCTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 2
AAF25730
ID AAF25730 standard; DNA; 1467 BP.
XX AC AAF25730;
XX DT 06-APR-2001 (first entry)
XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.
XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
XX KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
XX KW cosmetic; ds.
XX OS Ceratodon purpureus.
XX FH Key Location/Qualifiers
XX FT CDS 10..1461
XX FT /*tag= a
XX FT /product= "delta6-acetylenase/delta6-desaturase"
XX PN WO200075341-A1.
XX PD 14-DEC-2000.
XX EF 07-JUN-2000; 2003WO-BP005274.
XX PR 07-JUN-1999; 93DE-01025718.
XX PR 22-DEC-1999; 93DE-01062409.
XX PA (BADI ) BASF AG.
XX PI Heinz E, Styne S, Lee M, Girke T, Sperling P, Zaehrerger U;
XX WPI; 2001-112150/12.
XX DR P-PSDB; AMS46436.
XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX PT producing plant oils with increased content of unsaturated fatty acids.
XX PS Claim 1a; Page 46-48; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
XX CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
XX CC activity. The invention also describes (a) amino acid sequences encoded
XX CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
XX CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
XX CC organisms containing (I), EC or the vectors of (c); (e) preparation of
XX CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
XX CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
XX CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
XX CC production of (A) or TG by using (IIa); and (h) (A) and TG produced by
XX CC method (g). (I) are used to produce transgenic plants (or other
XX CC organisms) that produce oils or triglycerides (TG) with increased content
XX CC of unsaturated fatty acids (A) and to isolate related sequences by
XX CC homology screening. (A), or TG containing them, are useful in human
XX CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
XX CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
XX CC be used to suppress expression of (II), resulting in oils with increased
XX CC content of saturated fatty acids

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SQ Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;
Query Match 71.4%; Score 1456.4; DB 4; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 171 CAAAATGCGCCCTGCTTACCGACTTTCTGAACCTTTCTGGGCACGACATGGAGCAAGTACA 230
Db 5 CAAAATGCGCCCTGCTTACCGACTTTCTGAACCTTTCTGGGCACGACATGGAGCAAGTACA 64
QY 231 GCGGTGACACCCATAGCTATGCTGGAACCTATGGGCTACTTTTGAAGCAGCCCAAAAGG 290
Db 65 GCGGTGACACCCATAGCTATGCTGGAACCTATGGGCTACTTTTGAAGCAGCCCAAAAGG 124
QY 291 TTTCTGCTCAAGGTAAACCTGCGGGACAGACACTGAGACAGAGATCGGTGACGACAAA 350
Db 125 TTTCTGCTCAAGGTAAACCTGCGGGACAGACACTGAGACAGAGATCGGTGACGACAAA 184
QY 351 AGCCAGGCACTTACTCTCTGCGCGATGTTGCTTCTCAGCAGCGCTTGAGAGCTGTGGA 410
Db 185 AGCCAGGCACTTACTCTCTGCGCGATGTTGCTTCTCAGCAGCGCTTGAGAGCTGTGGA 244
QY 411 TGATCGTCAAGAGAGAGGTATGATATTAGCGGTTTTCGGGACGACCACTTGGAGGGA 470
Db 245 TGATCGTCAAGAGAGAGGTATGATATTAGCGGTTTTCGGGACGACCACTTGGAGGGA 304
QY 471 CGGTAATTAGCACTTACTTTTGGCGGGATGGCAAGACGTTTTCGCAACATTCATCCAC 530
Db 305 CGGTAATTAGCACTTACTTTTGGCGGGATGGCAAGACGTTTTCGCAACATTCATCCAC 364
QY 531 CTGCGCGATGGAGAACTCAATGACTACTACATTGGAGACCTTGTAGGAGAGAGCCCC 590
Db 365 CTGCGCGATGGAGAACTCAATGACTACTACATTGGAGACCTTGTAGGAGAGAGCCCC 424
QY 591 TTGATGAATTGCTTAAAGACTACAGAGATATGAGCCGAGTTTGTAGAGAGAGGCTTT 650
Db 425 TTGATGAATTGCTTAAAGACTACAGAGATATGAGCCGAGTTTGTAGAGAGAGGCTTT 484
QY 651 TCAAGAGTTTCCAGGCGCTGCTTCTGCTTCTGACTCTGATTAATGAGCTCTCTTTGCTG 710
Db 485 TCAAGAGTTTCCAGGCGCTGCTTCTGCTTCTGACTCTGATTAATGAGCTCTCTTTGCTG 544
QY 711 CGAGCATTCGCACTATCTGTTACGACAGAGTTTCTGGGCTATGCTGTGAGCAGTT 770
Db 545 CGAGCATTCGCACTATCTGTTACGACAGAGTTTCTGGGCTATGCTGTGAGCAGTT 694
QY 771 TGATGGTCTCTTCGTCGCAACAGTGTGATGGCTTCCCATGATTTCTTCTCATCAACAGG 830
Db 605 TGATGGTCTCTTCGTCGCAACAGTGTGATGGCTTCCCATGATTTCTTCTCATCAACAGG 664
QY 831 TCTTTGAGAACCGTACCGGAACTCCTTCTTTGGCTATTGTTTCGCAATTTGGCTGTG 890
Db 665 TCTTTGAGAACCGTACCGGAACTCCTTCTTTGGCTATTGTTTCGCAATTTGGCTGTG 724
QY 891 GCTTTAGTCTATCATGTTGGAGGACGAGCAACATTCATCATCTGCTCCGAATGAGT 950
Db 725 GCTTTAGTCTATCATGTTGGAGGACGAGCAACATTCATCATCTGCTCCGAATGAGT 784
QY 951 GCGAGCAACAGTACACACCTCTAGACGAGCAATTTGATACTCTCCCATCATTCGCTGGA 1010
Db 785 GCGAGCAACAGTACACACCTCTAGACGAGCAATTTGATACTCTCCCATCATTCGCTGGA 844
QY 1011 GCAAGGAAATTTGGCCACCGTTGAGAGCAAGAAATTTTGGAGTGCTTCAATATCAGC 1070
Db 845 GCAAGGAAATTTGGCCACCGTTGAGAGCAAGAAATTTTGGAGTGCTTCAATATCAGC 904
QY 1071 ACTACATGATCTGCTCTTATTTGTCGCGCGTACAGTTGGAGTTTGGAGTTTGC 1130
Db 905 ACTACATGATCTGCTCTTATTTGTCGCGCGTACAGTTGGAGTTTGGAGTTTGC 964
QY 1131 TCTTCACATTCATCTGATTTGAGCAGCAACCAAGGATTTGATAGAGAGGGAACAGTTG 1190
Db 965 TCTTCACATTCATCTGATTTGAGCAGCAACCAAGGATTTGATAGAGAGGGAACAGTTG 1024

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Db      1058  CACACGATGATGGGATTTGATCTCTCCCATCATTCCTGGAGTAAGATCTCTT 1117
Qy      1024  GGCACCGTTGAGACCAAGAGATTTTGGAGTGTCTCAATATCAGCACTACATGATCTT 1083
Db      1118  GGCACCTGTGAGAGCAAGACCATGTTGGAGTCTTTCAGTACCAAGCACTATCTTTT 1177
Qy      1084  GCTCTATGTTCTATGCGCCGGTACAGTTGGACTTTTGAAGTTGCTCTTACATCAA 1143
Db      1178  GCTTCTTTTGACGTTTGCCCGGGCGAGTTGGCTATTTTGGAGCGCGCCCTTCACTCTAG 1237
Qy      1144  TCTGATTTGACACAGCAACAGGATTCATAGAGAGGCAAGTGTCTTTTCACTACGC 1203
Db      1238  GGCAGGTTGACCTTGGCGAGAGCTTTTGAGAGGGGAAAGATGCTTTGCACTACAT 1297
Qy      1204  CTGGTTCAGTTGGGTCGTTCCATATTTTGGCGGTTGCGTAAAGCTTCTGCGTGGAT 1263
Db      1298  TTGGCTTAATAGTGTTCGCTTTTATCTGCTCCCGG--ATGMAAACAGTTGTATGGAT 1354
Qy      1264  GTAGCACTGAGCTTGTGGCGGTTTGTGTTGGATTCGTTGTTTACGTTGAGTACAA 1323
Db      1355  GTGTGTCAGCGAGCTCATGTCTGTTTCTGCTGGGATACGTTATTTGTACTCAGTCAAA 1414
Qy      1324  TGGAAAGGAGGTTTACAATGAATCGAAGGACTTCGTGAGAGCCAGGTTTATACCAACCG 1383
Db      1415  TGGATGAGGTTGATACATACGTCAGAGGACTTGTGATGCCAGATTCGATGACTCG 1474
Qy      1384  TAACACAGGAGGCTGTTCAAGATTTGTTCTACCTGGGAGCTCGACACCCAGATTGA 1443
Db      1475  CGACATCAAGACGCGGTTTAAATGATTTGTTTCCCGAGGCTCAACAGACAGATTGA 1534
Qy      1444  GCATCAGCTGTTTCAACAAATGCCAGGACCACTACCCAGATCGGACCTCAGTGA 1503
Db      1535  GCATCATCTATTTCAACAGATGCCAGGACCACTTAAATAAATTTCTCTCAGCTGA 1594
Qy      1504  GCTCTTTTGAAGACGAGCGCTCGATGATGATGATGCTCGGTTGTTGCTGCTGCT 1563
Db      1595  GACTTGTGCAAGAGCATGACTGTTTACAGAGCTGAGCATGGCTTCGGGCACTTA 1654
Qy      1564  CGCGTTGTGAAGCGCTCAAGAAATTTGCTGATGAAGCTCAATTCGGCTTCAAGCT 1621
Db      1655  CCGGTTTGTAAACACTTAAGAGCTTGCCGATGCTGCTTACACACGAGCAGCTTGT 1712

RESULT 4
ABV74260
ID      ABV74260 standard; cDNA; 1578 BP.
XX      AC      ABV74260;
XX      DT      28-MAR-2003 (first entry)
XX      DE      Physcomitrella patens desaturase encoding cDNA SEQ ID NO 7.
XX      KW      Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
XX      KW      animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
XX      KW      gene; ss.
XX      OS      Physcomitrella patens.
XX      FH      key      Location/Qualifiers
XX      CDS      1..1578
XX      FT      /*tag= a
XX      ET      /product= "desaturase"
XX      DE      0102337-A..
XX      PD      25-JUL-2002.
XX      PF      19-JAN-2001; 2001DE-01002337.
XX      PR      19-JAN-2001; 2001DE-01002337.
XX

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PA      (BADI ) BASF PLANT SCI GMBH.
XX
PI      Lerchl J, Renz A, Heinz E, Damerque F, Zaehring U;
XX      WPI; 2002-644810/70.
DR      P-PSDB; ABS98277.
XX
PT      Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT      animal or human nutrition, by transforming organism with desaturase gene
PT      from Phaseodactylum tricornutum.
XX
PS      Example 16; Page 60-63; 182pp; German.
XX
CC      The invention relates to preparing (MI) fatty acid esters (I) with an
CC      increased content of polyunsaturated fatty acids (II) with at least two
CC      double bonds by introducing into a (I)-producing organism a specific
CC      nucleic acid (A). (MI) is useful for preparing ester containing
CC      polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC      produced by (MI) are used in animal and human nutrition, cosmetics and
CC      pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC      the blood and to protect against heart disease. Cells that express (A)
CC      are also used to identify (ant)agonists of desaturases, e.g. for
CC      modulating the yield and rate of production of particular fine chemicals
CC      in microorganisms (claimed). Also (A) and derived proteins can be used as
CC      markers of specific genomic regions and in evolutionary/protein
CC      structural studies. (MI) is suitable for large scale production (no known
CC      bioengineering method can produce (II) on a useful scale). The present
CC      sequence is that of a Physcomitrella patens desaturase encoding cDNA used
CC      as the (A) component of the invention in producing transgenic (I)-
CC      producing organisms
XX
SQ      Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;

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Query Match      27.8%; Score 567.4; DB 6; Length 1578;
Best Local Similarity 66.3%; Pred. No. 3.8e-130;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

Qy      359  ACTTACTCTCTGGCGATGTTGCTTCTCAGCAGAGCCCTGGAGACTGCTGGATGATCGTC 418
Db      310  ACACACCCCTATCAGAGTAGCAGTACACAAACCAAGCGATTGCTGGATTGTGA 369
Qy      419  AAAGAGAGGTTGATGATATTAGCCGTTTTCGGACGACACCCCTGGAGGAGCGTAATT 478
Db      370  AAAACAGAGGTTGATGATGTTTCCAAATTTTCGGAGGAGCATCCCGAGATCAGTTATT 429
Qy      479  AGCAGCTACTTTGGCGGATGCGCAGACGATTTTCGCAACATTCATCCACCTGCCGCA 538
Db      430  AGTACTTATTTTGGAGAGAGCGCAGACAGATGTTTCTCTAGTTTTCATGAGCTTCTACA 489
Qy      539  TGGAGCGAAGCTCAATGACTACTACATTTGAGACCTTGTAGGAGAGAGCCCTTGTATGAA 598
Db      490  TGGAAAAATTTCTCAAGACTTTTACATTTGTCAGTGGAGGGTGGAGCGGACTCCAGAG 549
Qy      599  TTGCTTAAAGACTACAGAGATATGAGCGGAGTTTGTAGAGAGGGCTTTTCAAGAGT 658
Db      550  CTGCTGAAAGATTTCCGAGAAATGAGAGCTTTTCTCGAGGAGCAACTTTTCAAAGT 609
Qy      659  TCCAGGCGCTGGTCTCTGCTCAGACTCTGATTAATGAGCTCTCTTTCTCGAGCAATT 718
Db      610  TCGAAATTTGACTATGTTATGAAGCTGCTCAAGATTTGCTTATTTTCTCGAGCAATT 669
Qy      719  GCGACTATCTGTTACGACAGAGTTACTGCGCTATTTGCTGTCTGACAGCTTTGATGGCT 778
Db      670  GCAATAATATGTTGAGCAAGACTATTTTCAGCGGTTTGGCTTCAGCTTGTATGATGGCT 729
Qy      779  CTCCTCGCCAAAGTGTGGATGGCTGCTCCATGATTTCTTCATCAACAGAGCTCTTTGAG 838
Db      730  CTGTGTTTCCAAAGCTGCGGATGGCTATCCCATGATTTTCCCAATCAGAGTGTGAG 789
Qy      839  AACCGTACCGGAACTCCTCTTTGGCTATTGTTTGGCAATTTGCTTGGCTTTAGT 898
Db      790  ACAGCTGGCTTAATGAAGTTTGTGGGTATGTGATCGGCAAGCGGCTTCTGGGTTTACT 849

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Db 730 CTGTGTTTCCACAGTGGGATGCTATCCCATGATTTTCTCCCAATCAGGTGTTGAG 789
QY 839 AACCGTACCGCGAATCTCTTCTTGGCTATTGTTGCGCAATGCGTGTGCTTTAGT 898
Db 790 ACACGCTGGCTTAAAGAGTTGCGGTATGATCGCAAGCGCTTCTGCGTATTAGT 849
QY 899 GTATCATGTGTGAGAGCAAGACACACATTCATCTACTGCTCGGAATCAGTGGCGAA 958
Db 850 ACAGGTGTGTGAGAGAGAGCATACCTTTCATGCTGCTCCAAATGAATGCGATCAG 909
QY 959 CAGTACACACCTCTAGACGAGACATTTGATATCTCTCCCATCATCTGCGTGGAGAGGAA 1018
Db 910 ACTTACCAACCAATTTGATGAGATATTGATATCTCTCCCTCATTTGCTGGAGCAGGAC 969
QY 1019 ACTTGGGACCGTGTGAGAGCAAGAGATTTTGGAGTCTCTCAATATCAGCACTACATG 1078
Db 970 ATACTGGCCACAGTTGAGAAATAGACATTTCTGCGAATCTCCCAATACCAATCTGTT 1029
QY 1079 ACTTGGCTCTATTGTCATGCGCCGCTACATCTGCTGCTTTTGGAGTGTCTCTTCACA 1138
Db 1030 TCAATGGGCTGTTTATTTTCCCGGTGATGTTGCTCTTTTGGAGCTGGAGATATACC 1089
QY 1139 TCAATCTCTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGAGACAGTTGCTTTTAC 1198
Db 1090 TCTACAGCAGTCTCTCACTCTGACAGGTTGTTGAGAGAGGAACTGTTCTGTTTAC 1149
QY 1199 TACGCTGTGTCAGTTGGCTGCTTCCATATTTTGGCGGCTGCTGCTTAAAGCTCTTGG 1258
Db 1150 TACTTTTGGTTCGTCGGGACAGCTGCTATCTCTCCCTGCT---TGGAAAGCATTAGTA 1206
QY 1259 TGGATGTAGCACTGAGTGTGTCGCGTGTGTTGTTGGGATTTGTTGCTGTTAGTTGAGT 1318
Db 1207 TGGATGGCGGTGACTGAGCTCAATGTCGCGCATGCTGCTGGGCTTTGATTTGATCTTAC 1266
QY 1319 CACATGGAAGAGGATTTCAATCAATCGAAGGACTTCGTGAGAGCCGAGGTTATTACC 1378
Db 1267 CACATGGGATGGAGTTTATAATTCGTAAAGATTCGTGAGTGCAGATCGTATACC 1326
QY 1379 ACCGTATACACAGCGAGGTGTTCAAGTATGTTGCTGCTGGGAGCTGACACCGAC 1438
Db 1327 ACACGGGATATCAAGAGAAACATATTCACGACTGTTTCACTGCTGGGCTTTAAACGSCA 1386
QY 1439 ATTGAGCATCACTGTTTCCAAACATGCCAGGACACCTACCCCAAGATCGACCTCAG 1498
Db 1387 ATAGAGCATATCTTTTCCCAACATGCCAGGCAATATTTAAACAAATAGCACTAGA 1446
QY 1499 GTCAGGCTCTTTCAAGAACACGCGCTCGAGTACGATAATGCTCGTGTGTTGCTGCC 1558
Db 1447 GTGAGGTGTTCTGTAAGAAACAGGCTCTGTTGTACGAAGAGCTATCTATTGCTACCGGC 1506
QY 1559 TCTGTCGGGTTGAGGCGCTCAAGAAATGCTGATGAGCGTCAATTCGGGCTT 1615
Db 1507 ACTTGCAGGTTTGAAGCAATTGAAGGAAGTCGCGGAGGCTGCGGAGAGCAGCAT 1563

RESULT 6

AA26040

ID AAF26040 standard; cDNA; 2012 BP.

XX AC AAF26040;

XX AC AAF26040;

DT 23-APR-2001 (first entry)

DE P. patens delta6-desaturase cDNA.

XX Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
KW fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
KW agricultural chemical; ds.
XX Physcomitrella patens.

OS Physcomitrella patens.

XX Key Location/Qualifiers
FH 319..1896
FT CDS

/*tag= a
/product= "delta6-desaturase"

W0200102591-A1.

11-JAN-2001.

94-JUL-2000; 2000WO-EP006223.

06-JUL-1999; 99US-00347531.

30-JUN-2000; 2000DE-01030976.

(BADI) BASF AG.

Reinz E, Girke T, Scheffler J, Da Costa E SilvaO;

WPI; 2001-123117/13.

P-PSDB; AAB46810.

Production of unsaturated fatty acids, useful e.g. in nutrition,
cosmetics or pharmaceuticals, in organisms transformed with
Physcomitrella patens delta-6-desaturase nucleic acid.

Claim 1a; Page 38-41; 49pp; German.

This invention describes a novel preparation of unsaturated fatty acids
(-) by introducing into an organism at least one isolated nucleic acid
(II) that encodes a polypeptide (III) with Delta6-desaturase activity.
Organisms that contain at least 1 wt. % (I), on total fatty acid content,
are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
defined in the specification, or its equivalents within the degeneracy of
the genetic code; or (b) derivatives of the sequence of (a) that encode a
525 amino acid polypeptide (S2), defined in the specification, or a
polypeptide with at least 50% homology with (S2) and practically the same
enzymatic activity. The invention also describes (I) transgenic organisms
that contain (II); and (2) oils, lipids and fatty acids produced by the
new method. The oils, lipids and fatty acids produced by the transformed
organisms are used in human or animal nutrition, cosmetics,
pharmaceuticals and agricultural chemicals. (III) can also be used, in
vitro, for increasing the (I) content of triglycerides. The transgenic
organisms have increased contents of (I), or of (I)-containing
triglycerides, particularly of gamma-linolenic acid

Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 0 U; 0 Other;

Query Match

Best Local Similarity 27.8%; Score 567.4; DB 4; Length 2012;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGGCGGATGTTGCTTCTCAGCAGAGCCCTGGAGACTGCTGGATGATCGTC 418

Db 628 ACACACCCCTATCAGAAGTAGCAGTACACACCAAGCGATTGCTGGATTGTTGA 687

QY 419 AAAGAGAGGTGATGATATTAGCCGTTTTCGGAGACCACTCCCTGGAGGACGTAAT 478

Db 688 AAAACAAGGTGATGATGTTTCCAAATTTTCGGACGAGCATCCCGAGGATCAGTTATT 747

QY 479 AGCACTTCTTTGGCGGGATGGCAGACAGCTTTTGGCAACAATTCCTCCACTGCGCA 538

Db 748 AGTACTTATTTTGGACGAGACGCGACACAGATGTTTCTCTAGTTTTCATGCCAGTTCTACA 807

QY 539 TGGAGCACTCAATGACTACTATATTGAGACCTTGTGAGGAGAGCCCTTCAGAGAA 598

Db 808 TGGAAAATTTCTCAAGACTTTTACATTGTCAGCTGGAGAGGGTGGAGCCGACTCCAGAG 867

QY 599 TTGCTTAAAGACTACAGATATGAGACCGGAGTTTGTAGAGAGGGCTTTTCAAGACT 658

Db 868 CTGCTGAAAGATTTCCGAGAAATGAGAGCTCTTTTCTGAGGAGCAACTTTTCAAAAGT 927

QY 659 TCCAAGGCTGGTTCCTGCTTCAGACTCTGATTAATGAGCTCTCTTTGCTGGAGCAATT 718

Db 928 TCGAAATGTACTATGTTATGAAGCTGCTCAGATGTTGCTATTTTCTGCTGGAGCAATT 987


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QY 659 TCCAGGCGTGGTTCCTGCTTCAGACTCGATATATGACGCTCTCTTTGCTCGAGCAAT 718
Db 928 TCGAATTTGACTACTGTTATGAAGTGTCTACGAATTTGCTATTTTCTCGAGCAAT 987
QY 719 GCGACTACTGTTACGACAGAGTTACTGGGTATTTGCTGCTGACGCGATTTGATGGT 778
Db 988 GCAATAATATGTTGAGCGAGACTATTTTACGGGTTTGGCTTCAGCTTGTATGATGGCT 1047
QY 779 CTCCTTCGTCACACAGTGGATGGCTTGCCTATGATTTCTTCATCAACAGGCTCTTTGAG 838
Db 1048 CTGTGTTTCCAAACAGTGGGATGGCTATCCCATGATTTTCTCCAAATCAGGCTTTGAG 1107
QY 839 AACCGTACGGGAATCTCTTTGCTATTTTGTTCGCAATTTGGTTCGCTTTTGTAGT 898
Db 1108 ACACGCTGGCTTAATGAAGTTGTGCGGTATGATCGGCAACGCCGTTCTGCGGTTTGTAGT 1167
QY 899 GTATCATGTTGGAGGACGAGCAACATTCATCATCTGCTCCGAATGAGTGGACGAA 958
Db 1168 ACAGGCTGGTGGAGGAGAGCATACCTTCATCATGCTGCTCCAAATGAATGCGATCAG 1227
QY 959 CAGTACACACCTCTAGACGAGACATTCATCTCTCCCATCATTTCCCTGAGCAAGGAA 1018
Db 1228 ACTTACCAACCAATTTGATGAAGATTTGATCTCTCCCGCTCATTTGCCCTGGAGCAGGAC 1287
QY 1019 ATTTGGCCACGTTGAGAGCAGAGAAATTTGCGAGTGTCTCAATATCAGACATCATG 1078
Db 1288 ATACTGGCCACAGTTGAGAAATGAAGATTTCTTGGCAATCTCTCAATACGACATCTGTC 1347
QY 1079 ATTTGCTCTATTTGTCATGCCCCGATACAGTTCGACTTTTGGAAATTTGCTCTCA 1138
Db 1348 TTATGGCTGTATTTTTCGCCGTGTAGTGTGCTTTTGGAGCTGGAGATATACC 1407
QY 1139 TTCATCTCTATTTGACGACGACCAAGGATTTGATGAGAGGGAACAGTTCCTTTTCCAC 1198
Db 1408 TCTACAGCGTGTCTACCTCTGACAGAGTGTGAGAGAGGAACTGTTCTGTTTCCAC 1467
QY 1199 TACGCTGTTTTCAGTGGCTGCGTTCATATTTTGGCGGTGCTGCTAAGCTCTTGG 1258
Db 1468 TACTTTTGGTTCGTCGGGACAGCGTCTATCTCTCCCTGCT---TGGAGCCATTAGTA 1524
QY 1259 TGGATGTTAGCACTGACTGTGCGCGTTTGTGTTGGGATTCGTTTACGTTGAGT 1318
Db 1525 TGGATGCGGTGACTGAGCTCATGTCCGCGCATGCTGCTGGGCTTTGATTTGACTTACG 1584
QY 1319 CACATGGAAGAGGAGTTTACAAATGAAATGGAAGGACTTTGCTGAGAGCCGAGTTATACC 1378
Db 1585 CACAATGGGATGGAAGTTTATAATTCGCTAAAGAAATTCGTGAGTGCACAGATCGTATCC 1644
QY 1379 ACCGTTAACACACGCGAGGCTGTTCAACGATTTGTTCACTGGGGGACTGACACCCAG 1438
Db 1545 ACACGGATATCAAGGAAACATATTTCAACGACTGTTTCACTGGGCTTAAACAGGCAA 1704
QY 1439 ATTGAGCATCACTGTTTCCAAATGCTCCAGGCAACACTACCCCAAGATCGCACTCAG 1498
Db 1705 ATGAGCATCATCTTTTCCAAATGCTCCAGGCAACACTTAAACAAATAGCACTAGA 1764
QY 1499 GTCAGGCTCTTTGAGAGACGCGCTCGAGTACGATAATGTTCCGTTGCTGGTCC 1558
Db 1765 GTGAGGCTGTTCTGTAGAAACACGCTCTGTTGTAAGAAAGCTATCTATTGCTACCGGC 1824
QY 1559 TCTGTGCGGTTGTAAGGCGCTCAAGCAATTTGCTGATGAGCGTCAATTCGGCTT 1615
Db 1825 ACTTGCAGGTTTGAAGCAATTTGAAGGAAGTCCGCGAGGCTGCGGAGAGCGAT 1881
```

RESULT 8

ABV74274

ID ABV74274 standard; DNA; 15430 BP.

XX AC

XX ABV74274;

DT 07-AUG-2003

(revised)

```
DT 28-MAR-2003 (first entry)
XX Plant specific expression vector expressing desaturase SEQ ID NO 25.
XX Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW plant; elongase; gene; ds.
XX Phaeodactylum tricornutum.
OS Physcomitrella patens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
CDS 11543..12415
FT /*tag= a
FT /product= "elongase"
FT /note= "AB98278"
CDS 13313..14890
FT /*tag= b
FT /product= "desaturase"
FT /note= "AB98277"
DE10102337-A1.
PD 25-JUL-2002.
XX 19-JAN-2001; 2001DE-01002337.
XX 19-JAN-2001; 2001DE-01002337.
XX (BADI ) BASF PLANT SCI GMBH.
PA Lerchl J, Renz A, Heinz E, Damerque F, Zaehring U;
PI MPI; 2002-644810/70.
XX P-PSDB; AB98278, AB98277.
PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT animal or human nutrition, by transforming organism with desaturase gene
PT from Phaeodactylum tricornutum.
XX Example 11; Page 136-150; 182pp; German.
XX The invention relates to preparing (M1) fatty acid esters (I) with an
CC increased content of polyunsaturated fatty acids (II) with at least two
CC double bonds by introducing into a (I)-producing organism a specific
CC nucleic acid (A). (M1) is useful for preparing ester containing
CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC produced by (M1) are used in animal and human nutrition, cosmetics and
CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC the blood and to protect against heart disease. Cells that express (A)
CC are also used to identify (ant)agonists of desaturases, e.g. for
CC modulating the yield and rate of production of particular fine chemicals
CC in microorganisms (claimed). Also (A) and derived proteins can be used as
CC markers of specific genomic regions and in evolutionary/protein
CC structural studies. (M1) is suitable for large scale production (no known
CC bioengineering method can produce (II) on a useful scale). The present
CC sequence is that of the pUC19 based plant specific expression vector
CC (ABV74272) expressing the Physcomitrella patens elongase (AB98278) and
CC the Phaeodactylum tricornutum desaturase (AB98277) of the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;
```

Query Match

Best Local Similarity 27.8%; Score 567.4; DB 6; Length 15430;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGGCGATGTTGCTTCTCACGACGCGCTGGAGACTGCTGGATGATCGTC 418

Db 13622 ACACACCCCTATCAGAAGTAGCAGTACACACAGCCAGCGATTGCTGGATTCTGTA 13681

SQ Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3728 T; 0 U; 0 Other;
Query Match 27.8%; Score 567.4; DB 6; Length 15430;
Best Local Similarity 66.3%; Pred. No. 8.9e-130;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
QY 359 ACTTACTCTCGCCGATGTTGCTCTCAGCAGAGCCCTGGAGACTGCTGGATGACCGTC 418
Db 13622 ACACACCCCTATCAGAGTAGCAGTACACACAAAGCCCAAGGATTTGCTGGATTTGTA 13681
QY 419 AAAGAGAGGCTATGATGATAGCCGTTTTCGGAGCAGCACCCTCGAGGACGGTAAT 478
Db 13682 AAAACRAGGTGATGATGTTCCATTTTTCGGAGCAGCAGCAGCAGCAGCAGCAGTAT 13741
QY 479 AGCAGCTACTTTGGCGGGATGCGACAGAGCTTTTCGCAACATTCATCCACTGCGCGA 538
Db 13742 AGTACTTATTTGGACGAGCGCAGATGTTTCTCTAGTTTTCATGAGCTTCTACA 13801
QY 539 TGGAGCAACTCAATGACTACTACATTTGAGACCTTGCTAGGAGAGCCCTTGTATGA 598
Db 13802 TGGAAATTCCTTCAAGACTTTTACATTTGGTACGCTGGAGAGGCTGGAGCGGACTCCAGAG 13861
QY 599 TTGCTTAAAGACTACAGAGATAGAGCGGAGTTTGTAGAGAGGGCTTTTCAAGAGT 658
Db 13862 CTGCTGAAAGATTCGAGAAATGAGAGCTTTTCTCGGGAGCAACTTTTCAAGAT 13921
QY 659 TCCAGGCGCTGCTCTGCTCAGACTCTGATTAAGCAGCTCTTTCTGCTGGAGCATT 718
Db 13922 TCGAAATTTACTATGTTATGAAGTGTCTCAGAAATGTTGCTATTTTCTGCGAGCAT 13981
QY 719 GCGACTATCTGTACGAGAGTATACGGGTATTTGCTGTGACCGAGTTTGAGGGT 778
Db 13982 GCAATATATGTTGAGCAAGCACTATTTGAGCGGTTTGGCTTCAGCTTGTATGAGGCT 14041
QY 779 CTCCTCGTCCACAGTGTGGAATGCTGTCCTGATTTCTTCATCAACAGGCTTTTGAG 838
Db 14042 CTGCTGTTTCCACAGTGGGATGCTATCCCATGATTTTCCCAATCAGGTTTGTAG 14101
QY 839 AACCGTACCGGAACTCTTCTTCTGCTATTTGTTGCGGAATTTGCTGCTGCTTTAGT 898
Db 14102 ACACGCTGCTTAATGAAGTTCTCGGTATGATCGCAACGCTTCTGCGGTTTGTAG 14161
QY 899 GTATCATGCTGAGAGCAGAGCAGACATTCATCATCTGCTCGGAATGAGTGCAGGAA 958
Db 14162 ACAGGCTGTTGGAAGAGAGCAATACCTTCATCATGCTGCTCCAAATGAATGCGATCAG 14221
QY 959 CAGTACACCTCTAGACAGACATTTGATATCTCTCCCATCATTTGCTCGAGCAAGGAA 1018
Db 14222 ACTTACCAACCAATTTGATGAAGATTTGATATCTCTCCCATCATTTGCTCGAGCAAGGAA 14281
QY 1019 ATTTTGGCCACCGTTGAGAGCAGAGAAATTTGCGAGTGTCTCAATATCAGCACTACATG 1078
Db 14282 ATACTGGCCACAGTTGAGAAATGAAGATTTCTTGGCAATCTTCCAAATACCAATCTGTTTC 14341
QY 1079 ATCTGCTCTATTTGTCATGCGCGGTACAGTTGCACTTTTGGAGTTGCTCTTCA 1138
Db 14342 TFCATGGGCTGTTATTTTTCGCGGTGTTAGTGTCTCTTTTGGAGCTGGAGATATACC 14401
QY 1139 TFCATCTCTGATTTGAGCAGCAGCAGGAGTGTATAGAGAGGAAACAGTTGCTTTTCA 1198
Db 14402 TCTACAGCAGTGTCTCTACCTGTGACAGAGTTGTTGGAGAGGAACTGTCTGTTTCA 14461
QY 1199 TAGGCTGTGTTGAGTGGCTGCTGCTATTTTTCGCGGTGCTGCTAGGCTCTTGGG 1258
Db 14462 TACTTTGCTGCTGCGGACAGGCTGCTATCTTCTCCCTGCT---TGGAGAGCAATTAGTA 14518
QY 1259 TGGATGTTAGCACTGAGCTTGGCGGCTTGTGTTGCTGGATTCGTTTACGTTGAT 1318
Db 14519 TGGATGCGGCTGACTGAGCTCATGTCGCGCATGCTGCTGGCTTTTGTATTTGTTACTAG 14578
QY 1319 CACAATGGAAGAGGTTTACCAATGAATCGAAGGACTTGTGAGAGCCAGGTTTATACC 1378
Db 14579 CACAATGGATGGAGTTTATANTTGTCTAAGAAATTCGTGAGTGCAGATCGTATCC 14638

QY 1379 ACCGTAAACACGAGGAGGCTGTTCAACAGTATGTTGTTACTGGGGACTCGACCCAG 1438
Db 14639 ACACGGGATATCAAGGAAACATATTTCAACGACTGTTCACTGTTGCTTTAAACGGCAA 14698
QY 1439 ATTGAGCATCACTGTTTCCCAACATGCCAGGCACTTACCCCAAGATCGACCTCAG 1498
Db 14699 ATAGAGCATCATCTTTTCCCAACATGCCAGGCACTTATTTAAACAAATAGACCTAGA 14758
QY 1499 GTGAGGCTCTTTTGCAGAGCAGCAGCGCTCGAGTACGATAATGTTCCGTTGTTGGTCC 1558
Db 14759 GTGAGGCTCTTCTGTAAAGAAACAGCGTCTGGTGTACGAGACGTATCTATTGCTACCGGC 14818
QY 1559 TCTGTGCGGCTGTTGAGGCGCTCAAGGAAATTTGCTGATGAAGCTCAATTCGGCTT 1615
Db 14819 ACTTGAAGGTTTGAAGCATTTGAAGGAAATTCGAGGAGCTCGGAGGCTCGGAGAGCAT 14875
RESULT 10
ABV74275
ID ABV74275 standard; DNA; 17752 BP.
XX
AC ABV74275;
XX
AC AC (revised)
DT 07-AUG-2003 (first entry)
DT 28-MAR-2003 (first entry)
DE
DE
XX Plant specific expression vector expressing desaturase SEQ ID NO 28.
KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW plant; elongase; gene; ds.
XX
OS Phaeodactylum tricornutum.
OS Physcomitrella patens.
OS Synthetic.
OS Chimeric.
XX
Key Location/Qualifiers
CDS 11543..12415
FT /tag= a
FT /product= "elongase"
FT /note= "ABB98273"
CDS 13313..14890
FT /tag= b
FT /product= "desaturase"
FT /note= "ABB98277"
CDS 15791..17200
FT /tag= c
FT /product= "desaturase"
FT /note= "ABB98274"
XX
DE10102337-A1.
XX
XX 25-JUL-2002.
XX
PF 19-JAN-2001; 2001DE-01002337.
XX
PR 19-JAN-2001; 2001DE-01002337.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Lerchl J, Renz A, Heinz E, Damerque F, Zaehring U;
XX
XX WPI; 2002-644810/70.
DR P-PSDB; ABB98278, ABB98277, ABB98274.
XX
XX Preparing ester containing polyunsaturated fatty acids, useful e.g. in
XX animal or human nutrition, by transforming organism with desaturase gene
XX from Phaeodactylum tricornutum.
PS Example 11; Page 154-170; 182pp; German.
XX

CC The invention relates to preparing (M1) fatty acid esters (I) with an
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing
 CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (c-aimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC bioengineering method can produce (II) on a useful scale). The present
 CC sequence is that of the pUC19 based plant specific expression vector
 CC (ABV74273) expressing the Physcomitrella patens elongase (ABB98278) and
 CC the Phaeodactylum tricornutum desaturase (ABB98277 and ABB98274) of the
 CC invention. (Updated on 07-AUG-2003 to correct OS field.)
 XX

SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;

Query Match 27.8%; Score 567.4; DB 6; Length 17752;
 Best Local Similarity 66.3%; Pred. No. 9.3e-130;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGCGCGATGTGCTCTCAGCAGAGCGCTGGAGACTCTCGATGATCGTC 418
 DB 13622 ACACACCCCTATCNGAAGTAGCAGTACACAAAGCCAGCGATTGCTGGATGTGTGA 13681
 QY 419 AAAGAGAGAGTGTATGATATTAGCGGTTTGGCGACACACCTCGAGGAGCGTAATT 478
 DB 13682 AAAAAAGAGTGTATGATTTTCCAAATTTTGGCGACAGCATCCGAGGATCAGTATT 13741
 QY 479 AGCACCCTACTTGGCGGGGATGGCAGACAGCTTTTCCAAATTCATCCACCCTGCCGA 538
 DB 13742 AGTACTTATTTTGGACGAGCGCACAGATGTTTCTCTAGTTTTCATCGAGCTTCTACA 13801
 QY 539 TGGAGCACTCATGCTACTACTATTGAGACCTTCTAGGAGAGAGCCCTTGATGA 598
 DB 13802 TGGAAATTTCTCAGACTTTTACATTGGTGAGCTGGAGAGGGTGGAGCGGACTCCAG 13861
 QY 599 TTCTTAAAGACTACAGAGATATGAGAGCGGAGTTTGTAGAGAGGGCTTTTCAAGAGT 658
 DB 13862 CTGCTGAAGATTTCGAGAAATGAGAGCTTTTCTCTGAGGAGCAACTTTCAAAGT 13921
 QY 659 TCCAGCGCTGGTTCCTGCTTGAGACTCTGATTAATGCACTCTCTTTCTGCGAGCAT 718
 DB 13922 TCGAAATTTGCTATGTTATGAAGCTGCTCAGCAATGTTGCTATTTTGTGCGAGCAT 13981
 QY 719 GCGACTATCTGTTACGACAGAGTTACTGGGCTATTGCTGTCAGCCAGCTTTGATGGGT 778
 DB 13982 GCAATACNIGTTGGAGCAAGACTATTTAGCGGTTTGGCTTCAGCTTGATGATGGCT 14041
 QY 779 CTCTTGGTCCAAAGTGTGGATGGCTTGGCCATGATTTCTTCATCAACAGGCTTTTGG 838
 DB 14042 CTGTGTTTCCAAAGTGGGATGGCTATCCATGATTTTCTCCAAATCAGGTTTGG 14101
 QY 839 AACCGTACCGGCACTCTCTTTGGCTATTGTTGGCAATTTGGCTGCTTGGCTTTAGT 898
 DB 14102 ACACGCTGGCTTAATGAAGTTGTGGGTATGTGATCGGCAACCGCTTCTGGGTTTGT 14161
 QY 899 GTATCATGTTGGAGGAGCAAGCAACATTCATCATCTCTCGAATGATGCGAGAA 958
 DB 14162 ACAGGTGGTGGAGGAGGAGCATAACTTCATCATGCTGCTCAATGATGGATCAG 14221
 QY 959 CAGTACACACTCTTAGACGAGACATTGATGATCTCTCCCATCATTTGCTCGAGCAAGAA 1018
 DB 14222 ACTTACCAACCAATTGATGAAGATATTGATGATCTCTCCCTCATTTGCTGAGCAAGGAC 14281
 QY 1019 ATTTTGGCCACCGTTGAGACAGAGAAATTTTGGAGTGTCTCAATATCAGCACTCATG 1078
 DB 14282 ATACTGGCCACAGTTGAGATATAGACATTTCTGCGAATCTCTCAATACCAAGCATCTGTC 14341

QY 1079 ATTCTGGCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGAAGTTGCTCTTCCACA 1138
 DB 14342 TTCTATGGGCTCTGTTATTTTTCGCCCGGTGGATGGCTCTTTTGGAGCTGGAGATATACC 14401
 QY 1139 TTCAATCTCTATTGAGCAGCAGCAACAGGGATTGATAGAGAGGAGCAAGTTGCTTTTCCAC 1198
 DB 14402 TCTACAGCACTGCTCTCACCTGTGCAGAGTTGTTGAGAGGAGCAAGTTGCTTTTCCAC 14461
 QY 1199 TAGCCCTGTTTCAAGTTGGGCTGGCTTCCATATTTTTCGGGCTGTCGCTTACGCTTTCGG 1258
 DB 14462 TACTTTTGGTTCGTTCGGGACAGCGTGTCTTCTCTCCCTGGT---TGGAAAGCCATTAGTA 14518
 QY 1259 TGGATGTTAGCACTGAGCTTGTGGCGGCTTGTGTTGTTGGATTTCGTTGTTTACGTTGAGT 1318
 DB 14519 TGGATGCGGCTGACTGAGCTCATGTCGCGCATGCTGCTGGCTTTGTTTGTACTTAGC 14578
 QY 1319 CACAATGGAAGAGGTTTACAATGAATCSAAGGACTTCGTTGAGAGCCCGAGTTTATTACC 1378
 DB 14579 CACAATGSGATGGAGGTTTATAATTCGTTCTAAAGAAATTCGTGAGTGCACAGATCGTATCC 14638
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 DB 14639 ACACGGGATATCAAGAGGAAACATATTCACGACTGTTCACTGGTGGCTTAAACAGCAA 14698
 QY 1439 ATTGAGCATCACCTGTTTCCAAACAATGCCAGGCACAACTACCCCAAGATCGCACCTCAG 1498
 DB 14699 ATGAGCATCATCTTTTCCCAACATGCCAGGCACTAATTTAAACAATAAGCACTTAGA 14758
 QY 1499 GTCGAGCTCTTTTCCAAAGACAGCGCTTCAGTACGATTAATGTTCTCGGTGTTGGTGCC 1538
 DB 14759 GTGAGGTTTCTGTAAAGAACACGCTTCGTTGTTACGAAGACGTTATCTATTGCTACCGGC 14818
 QY 1559 TCTGTGCGGCTTGTGAGGCGCTCAAGGAAATTCGTGATGAAGCGTCAATTCGGCTT 1615
 DB 14819 ACTTGCAAGCTTTTGAAGCAATTTGAAGAAAGTCGGAGGCTCGGAGAGCAGCAT 14875

RESULT 11

ABQ76797
 ID ABQ76797 standard; DNA; 17752 BP.

XX AC ABQ76797;

XX AC (first entry)

XX 25-MAR-2003

XX pBAR1 encoding delta6 elongase, delta6 and delta5 desaturase.

XX Promoter; expression cassette; structural gene; plant; transgenic;
 XX linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 XX animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 XX heart disease; seed-specific; ds.

XX Physcomitrella patens.

OS Phaeodactylum tricornutum.

OS Synthetic.

PH Key Location/Qualifiers

FT CDS 11543..12415

FT /*tag= a

FT /product= "delta6 elongase"

FT /note= "from Physcomitrella patens"

FT CDS 1313..14890

FT /*tag= b

FT /product= "delta6 desaturase"

FT /note= "from Physcomitrella patens"

FT CDS 15791..17200

FT /*tag= c

FT /product= "delta12 desaturase"

FT /note= "from Phaeodactylum tricornutum"

XX DE10102338-A1.

XX 25-JUL-2002.

PD

XX 19-JAN-2001; 2001DE-01802338.
 PF XX
 PR XX
 XX 19-JAN-2001; 2001DE-01802338.
 XX (BADI) BASF PLANT SCI GMBH.
 FA Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
 FI WPI; 2002-675961/73.
 XX P-PSDB; ABG73608, ABG73609, ABG73610.
 DR XX
 DR XX
 XX New expression cassette for plant genes, useful for preparing transgenic
 PT plants that have increased production of polyunsaturated fatty acids.
 XX Example 13; Page 158-174; 188pp; German.
 XX This invention describes novel expression cassette (EC) containing at
 CC least one each of plant promoter (P) and structural gene (SG) expressed
 CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
 CC The EC has the structure (U1-P-SG-L2) n where L1 = is a polylinker
 CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
 CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
 CC sequences and n = 1-3. The invention discloses a vector containing this
 CC EC, an organism containing the EC or the vector and a transgenic plant
 CC containing a (non-)functional nucleic acid in the vector. Transgenic
 CC plants e.g. line seed can be prepared with improved production of fatty acid
 CC esters with an increased content of polyunsaturated fatty acids (PUFA),
 CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
 CC PUFA are known to reduce levels of cholesterol in the blood and to
 CC protect against heart disease. The expression cassettes of the invention
 CC provide increased and more efficient production of fine chemicals
 CC (especially PUFA), including seed-specific production. This sequence
 CC represents a nucleic acid sequence used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 17752 BP; 4334 A; 4385 C; 4566 G; 4367 T; 0 U; 0 Other;
 Query Match 27.8%; Score 567.4; DB 6; Length 17752;
 Best Local Similarity 66.3%; Pred. No. 9.3e-130;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
 QY 359 ACTTACTCTCTGGCGATGTTGCTTCTCAACAGACGGCTGGAGACTGCTGGATGTCGC 418
 DB 13622 ACACACCCCTATCAGAGATGACAGTACACACAGCCAGCCAGGATGCTGGATTGTGTA 13681
 QY 419 AAGAGAGAGGTGATGATTAATAGCCGTTTTCGGACGACACCCCTGGAGGACGCTAAT 478
 DB 13682 AAAAAACAGGTGATGATGTTTCCNATTTTGGGACGAGCATCCGGAGGATCAGTTATT 13741
 QY 479 AGCACCTACTTTGGGCGGATGAGCAGACAGCTTTTTCGCAACATTCATCCACCTGCCGCA 538
 DB 13742 AGTACTTATTTTGGACGAGAGCGGACAGATGTTTCTCTAGTTTTCATGCGAGCTCTACA 13801
 QY 539 TGGAGGCACTCAATGACTACTACTATTGAGACCTTCTAGGAGAGCCCTTCATGATCA 598
 DB 13802 TGGAAATCTTCAAGATCTTTTACATGTTGACGTTGAGAGAGGAGCGGAGCTCCAGAG 13861
 QY 599 TTGCTTAAAGACTACAGATATCAGAGCCGAGTTTGTATGAGAGAGGCTTTTCAAGAGT 658
 DB 13862 CTGCTGAAGATTTCCGAGAAATGAGAGCTCTTTTCTGAGGAGCACTTTTCAAGAT 13921
 QY 659 TCCAGGCTCTGCTCTCTAGACTCTGATTAATGAGCTCTCTTTGCTGCGAGCAATT 718
 DB 13922 TCGAAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13981
 QY 718 GCGACTACTCTGACGAGCAAGATGACTGGGCTATGCTGCTGAGCCAGTTGATGGT 778
 DB 13982 GCAATAATATGTTGGAGCAAGACTATTTTCAAGCGGTTTGGCTTCACTGTGATGATGCT 14041
 QY 779 CTCTCGTCCCAACAGTGGGATGGCTTGGCCATGATTTCTTCTCATCAACAGCTCTTCGAG 838
 DB 14042 CTGTGTTCCAAAGTGGGATGGCTATCCCATGATTTCTTCCCAATCAGGTGTTGAG 14101

QY 839 AACCTACCGCAACTCCTCTTTGGCTATTGTTTGGCAATGCTGCTGCTTGGCTTAGT 898
 DB 14102 ACACGCTGGCTTAATGAAGTTCTCGGATGATGATCGGACGCGCTTCTGGGTTTAGT 14161
 QY 899 GTATCATGCTGGAGGAGCAACACATTCATCTACTACTGCTCCGATCAGTGCAGCA 958
 DB 14162 ACAGGCTGGAGGAGCAACATACCTTCATCTACTGCTCCCAATGAATCGATCAG 14221
 QY 959 CAGTACACACCTCTAGAGCAAGACATTCATCTCTCCCATCATTCCTTGGAGCAAGAA 1018
 DB 14222 ACTTACCAACCAATGATGAGATTAATGATCTCTCCCTCATTCCTTGGAGCAAGAA 14281
 QY 1019 ATTTTGGCCACCGTTGAGAGCAAGAAATTTTGGAGTCTTCAATATCAGACATCAGT 1078
 DB 14282 ATACTGGCCACAGTTGAGAAATGAACATTTCTTGGCAATCTTCAATACCAATCTGTT 14341
 QY 1079 ATTTGCTCTTATTGTTTATGCTGCGGCTACAGTTGAGACTTTTGGAGTTTCTCTACA 1138
 DB 14342 TTCTGCTGCTGTTTATTTTTCGCGGCTGATGATGCTCTTTTGGAGCTGGAGATATAC 14401
 QY 1139 TTCAATCTCTGATTTTTCAGCAACCAAGGATTTGATAGAGAGGAAACAGTTGCTTTTAC 1198
 DB 14402 TCTACAGAGTCTCTACCTGTCGACAGTTTGTGAGAGGAACTGTTCTGTTTTCAC 14461
 QY 1199 TACGCTGCTTACGTTGGCTGCTTCCATATTTTTCGCGGCTGCTGCTTAACTCTTGG 1258
 DB 14462 TACTTTTGGCTTCTGCTGGGACAGCTGCTATCTTCTCCCTGGT---TGGAGGCAATGTA 14518
 QY 1259 TGGATGTTAGCAACTGAGCTTGTGCGGCTTTTGTGTTGGGATTCGTTTACGTTGAGT 1318
 DB 14519 TGGATGCGGCTGACTGAGCTCATGTCGCGCTGCTGCTGGCTTTGATTTTGTACTAGC 14578
 QY 1319 CACAAATGAAAGAGGTTTACAAATGAATGAAAGGACTTCTGAGAGCCGAGGTTATTACC 1378
 DB 14579 CACAAATGGAATGAGGTTTATAATTCGTTAAAGAAATTCGTGAGTGCAGATCGTATCC 14638
 QY 1379 ACCGTTACACCAAGCGGCTGTTTCAAGATTTGTTCACTGGGAGCTCCACACCCAG 1438
 DB 14639 ACACGGATATCAAGAGGAAACATATTCACGCTGCTGCTGCTTAAACAGCA 14698
 QY 1439 ATTGAGATCACTCTTTTCCAAATGCCAGGCAACACTACCCCAAGATCGCACCTCAG 1498
 DB 14699 ATGAGGATCACTTTTCCAAATGCCAGGCAACACTTAAACAAATAGCACCTAGA 14758
 QY 1499 GTGAGGCTCTTTTCAAGAGCAAGCGCTTGGAGTACGATAATGTTCTCGTCTGTTGGTGC 1558
 DB 14759 GTGAGGCTCTTTTCAAGAAACACCGCTTGGTGTAGAGAGCTATCTATTGCTACCGGC 14818
 QY 1559 TCTGCTGGGCTTGTGAAGCGCTCAAGGAAATGCTGATGAAGCGTCAATTCGGCTT 1615
 DB 14819 ACTTGAAGGTTTGAAGAGCATTTGAAGAGTTCGCGGAGGCTGCGGAGAGCAGCAT 14875

RESULT 12

AAE25731
 ID AAE25731 standard; DNA; 520 BP.

XX
 AC AAE25731;
 DT 06-APR-2001 (first entry)

XX C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 5.
 DE Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic; ds.
 XX Ceratodon purpureus.
 OS WC200075341-A1.
 PN 14-DEC-2000.
 PD


```
XX PF 07-JUN-2000; 2000WO-EP005274.
XX PR 07-JUN-1999; 99DE-01025718.
XX PR 22-DEC-1999; 99DE-01062409.
XX PA (BADI ) BASF AG.
XX PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX DR WPI; 2001-112150/12.
XX DR P-PSDB; AAB46437.
XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX producing plant oils with increased content of unsaturated fatty acids.
XX Example 6; Page 51; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
XX polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
XX activity. The invention also describes (a) amino acid sequences encoded
XX by (I); (b) an expression cassette (EC) containing (I) linked to one or
XX more regulatory sequences; (c) a vector containing (I) and EC; (d)
XX organisms containing (I), EC or the vectors of (c); (e) preparation of
XX unsaturated fatty acids (A) or triglycerides (TG) with increased content
XX of (A) by introducing (I) or EC into an oil-producing organism; (f)
XX proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
XX production of (A) or TG by using (Ia); and (h) (A) and TG produced by
XX method (g). (I) are used to produce transgenic plants (or other
XX organisms) that produce oils or triglycerides (TG) with increased content
XX of unsaturated fatty acids (A) and to isolate related sequences by
XX homology screening. (A), or TG containing them, are useful in human
XX nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
XX cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
XX be used to suppress expression of (II), resulting in oils with increased
XX content of saturated fatty acids
XX SQ Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 0 U; 0 Other;

Query Match 25.4%; Score 518.4; DB 4; Length 520;
Best Local Similarity 99.8%; Pred. No. 3.5e-118;
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CATTTCATCTACTCTCGAATGAGTCGAGACAGCTACACCTCTAGACGAGACAT 984
DB 1 CATTTCATCTACTCTCGAATGAGTCGAGACAGCTACACCTCTAGACGAGACAT 60
QY 985 TGATACCTCTCCCATCTGCTCGAGCAGGAAATTTGGCCACCGTTGAGACGAGAG 1044
DB 61 TGATACCTCTCCCATCTGCTCGAGCAGGAAATTTGGCCACCGTTGAGACGAGAG 120
QY 1045 AATTTCCGAGTGTTCAATATGAGCTACTCATGATTCGCTCTATTGTTTCATGCGCCG 1104
DB 121 AATTTCCGAGTGTTCAATATGAGCTACTCATGATTCGCTCTATTGTTTCATGCGCCG 180
QY 1105 GTACAGTTGAGCTTTGGAGTTGCTCTTACATTCATCTGATTCGATTCGAGACGACAA 1164
DB 181 GTACAGTTGAGCTTTGGAGTTGCTCTTACATTCATCTGATTCGATTCGAGACGACAA 240
QY 1165 GGGATTGATAGAGGAGGAAAGTTGCTTTTTCATACGCTGTTGATTCGAGTTGGCTGGTT 1224
DB 241 GGGATTGATAGAGGAGGAAAGTTGCTTTTTCATACGCTGTTGATTCGAGTTGGCTGGTT 300
QY 1225 CCATATTTGCGGGTGTCCTAGCCTCTTCGCTGGATGATGATGATGATGATGATGATGAT 1284
DB 301 CCATATTTGCGGGTGTCCTAGCCTCTTCGCTGGATGATGATGATGATGATGATGATGAT 360
QY 1285 CGGTTGCTGTTGGAGTTGCTGTTTACGTTGAGTCACAAATGAAAGAGGTTTCAATGA 1344
DB 361 CGGTTGCTGTTGGAGTTGCTGTTTACGTTGAGTCACAAATGAAAGAGGTTTCAATGA 420
QY 1345 ATCGAAGACTTCGTGAGAGCCAGGTTTATACCAACCGTATACCAACCGTATACCAACCGT 1404
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Db 421 ACGAAGACTTCGTGAGAGCCAGGTTATTACACCCGTTACACAGCGAGGCTGGTT 480
QY 1405 CAACGATTGGTTCTACTCGGGGACTCGACACCCAGATTGAG 1444
Db 481 CAACGATTGGTTCTACTCGGGGACTCGACACCCAGATTGAG 520

RESULT 13
AAF25732
ID AAF25732 standard; DNA; 514 BP.
AC AAF25732;
XX 06-APR-2001 (first entry)
DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 7.
XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
XX transgenic plant; plant oil; triglyceride; nutrition; animal feed;
XX cosmetic; ds.
XX Ceratodon purpureus.
XX WO200075341-A1.
XX 14-DEC-2000.
XX 07-JUN-2000; 2000WO-EP005274.
XX 07-JUN-1999; 99DE-01025718.
XX 22-DEC-1999; 99DE-01062409.
XX (BADI ) BASF AG.
XX Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX WPI; 2001-112150/12.
XX P-PSDB; AAB46438.
XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX producing plant oils with increased content of unsaturated fatty acids.
XX Example 6; Page 51; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
XX polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
XX activity. The invention also describes (a) amino acid sequences encoded
XX by (I); (b) an expression cassette (EC) containing (I) linked to one or
XX more regulatory sequences; (c) a vector containing (I) and EC; (d)
XX organisms containing (I), EC or the vectors of (c); (e) preparation of
XX unsaturated fatty acids (A) or triglycerides (TG) with increased content
XX of (A) by introducing (I) or EC into an oil-producing organism; (f)
XX proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
XX production of (A) or TG by using (Ia); and (h) (A) and TG produced by
XX method (g). (I) are used to produce transgenic plants (or other
XX organisms) that produce oils or triglycerides (TG) with increased content
XX of unsaturated fatty acids (A) and to isolate related sequences by
XX homology screening. (A), or TG containing them, are useful in human
XX nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
XX cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
XX be used to suppress expression of (II), resulting in oils with increased
XX content of saturated fatty acids
XX SQ Sequence 514 BP; 115 A; 113 C; 137 G; 149 T; 0 U; 0 Other;

Query Match 12.5%; Score 254.6; DB 4; Length 514;
Best Local Similarity 69.6%; Pred. No. 7.4e-53;
Matches 360; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 925 CATTTCATCTACTCTCGAATGAGTCGAGACAGCTACACCTCTAGACGAGACAT 984
DB 1 CATTTCATCTACTCTCGAATGAGTCGAGACAGCTACACCTCTAGACGAGACAT 60
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QY 983 ATTGATCTCTCCCATCATTTCCCTGGAGCAAGAAATTTGGCCACCGTTGAGAGCAAG 1042
 Db 758 CTGTGACCTCGAGTGAGCATGGTGTGAGATGTTCTCGGATGTCCAGATGAGAGCTG 817
 QY 1043 AGAATTTTCCGAGTCTTCAATATACAGCACTACATGATCTCCCTCTATTTGTTATGTC 1102
 Db 818 ACCCGCATGTGTGCGTGTTCATGCTCCGAAACAGACCTGTTTATCTTCCCATTTCTC 877
 QY 1103 CGGTACAGTTCGACATTTTGGAGTTTGTCTTTCACATTTCAAT- 1144
 Db 878 TCGTTCGCGCTCTCTCTCGTGTGCTCCGATTCATCTTCTTGTCTGCTAAAGTCCAG 937
 QY 1145 -----CCTGATTTGAGCAAGCAAGGATTTGATAGAGAGGAGACAGTTGCT 1192
 Db 938 GCCCAAGCCCTCGGGCGCGGTGTGCTCCATCTCGTTGGTGGAGCAGCTGTGCTGCG 997
 QY 1193 TTTCACTACGCTGTTTCTGTTGGCTGCTTCCATATTTTTCGGGCTGCTAAAGCT 1252
 Db 998 ATGCACTGGATCTGTACTCTGCCACCATGTTCTTGTTCATCAAGATCCCGTCAACATG 1057
 QY 1253 CTTCGCTGGATGAGCAACTGAGCTTGTGGCGGTTTGTGTTGGGATTCGTGTTTACG 1312
 Db 1058 CTGGTGACTTTTGTGTGCGAGCGGTGTGCGGAAACTTGTGGCGATGCTGTTCTCG 1117
 QY 1313 TTGAGTCAATGGAAGAGGTTTACATGATGCTG-----AAGGACTTCGTG 1360
 Db 1118 CTCACCAACACGGTATCTGCTGTGATCTCGAAGGAGGCGCTCGATATGATTTCTTC 1177
 QY 1361 AGAGCCAGGTTATTACCAACCGTAACACCAAGCAGCGTGTCTCAACGATTGTTCACT 1420
 Db 1178 ACAGAGCAGATCATCAGCGGTGCTGATGTCCACCGGCTCTA-TTGCCAACTGGTTTACG 1237
 QY 1421 GGGGAGCTGACACCCAGATTGAGCATCACCTGTTTCCAAATCCCGAGCACAACATAC 1480
 Db 1238 GGTGAGTGAATATACATCAGATCAGACCACTTGTTCCTTCGATGCTCGCCACACTTT 1297
 QY 1481 CCCAGATGCGACCTCAGCTGAGGCTTTTCCAGAGCAGCGCTCGAGTACCATAT 1540
 Db 1298 TCAAGATCCAGCCCTGCTGTGAGACCTGTGCAAAAGTACAATGTCGATACCAACC 1357
 QY 1541 GTCTCCGCTGTTGGTCCCTCTGTCTGCGGTTGTGAAAGCGCTCAAGGAAATTCGTGATA 1600
 Db 1358 ACCGATATGATCGAGGAACTCGAGGCTTTTNGCGCTCTGACAGGCTCTCCAGGCT 1417
 QY 1601 CGGTCAATTCGCTTTCAGCTCAGCTCAGTAA 1631
 Db 1418 CCTCCAGATGGGTAGGCGCAGTAA 1448

RESULT 15

AA00889
 ID AA00889 standard; DNA; 1617 BP.

XX
 AC AA00889;

XX
 DT 26-MAR-1999 (first entry)

XX
 DE Mortierella alpina delta 6 desaturase encoding DNA.

XX
 KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; main nutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; ss.

XX
 OS Mortierella alpina.

XX
 FH Key Location/Qualifiers

XX
 CDS 71..1443

XX
 FT /*tag= a

XX
 FT /product= "delta 6 desaturase"

XX
 PW WO9846764-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US007421.
 XX
 PR 11-APR-1997; 97US-00833610.
 PR 11-APR-1997; 97US-00834033.
 PR 11-APR-1997; 97US-00834655.
 PR 24-OCT-1997; 97US-00956985.
 XX
 PA (CALT) CALGENE LLC.
 PA (ABBO) ABBOTT LAB.

XX
 PI Knutson D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
 PI Leonard AE;

XX
 WI 1999-080739/07.

XX
 P-PSDB; AAW95504.

XX
 PT Nucleic acid construct able to express fatty acid desaturase in plants -
 PT useful in human or animal nutrition, as cosmetics and therapeutically,
 PT e.g. for restenosis, cancer and diabetes.

XX
 PS Claim 1; Fig 3A-B; 210pp; English.

XX
 CC This DNA encodes a Mortierella alpina delta 6 desaturase. The invention
 CC relates to a nucleic acid construct that contains at least one of the
 CC nucleotide sequences (AA00889 to AA00891) encoding M. alpina delta 6,
 CC delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
 CC coupled to an expression control sequence functional in plants.
 CC Recombinant plant cells containing at least one DNA encoding a M. alpina
 CC fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA for their metabolites such as prostaglandins, e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
 CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish

XX
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

Query Match 7.5%; Score 153; DB 2; Length 1617;

Best Local Similarity 47.9%; Pred. No. 1.7e-27;

Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTCTGTGATGATCGTCAAGAGAGGTTGATGATATTAGCGGTTTCGGACGAC 457

Db 158 GCACCTTCTTGTGATGATCATCGACCAAGGTTAGGATGTCGCGAGTTCCTCTGAT 217

QY 458 CACCTCTGAGGAGCGGTAATTAGCACCTACTTTTGGCGGAGTGGCACAGACGTTTTCGA 517

Db 218 CATCCGCTGGAGTGTGATTTCTCAGCGACCTTGGCAAGGAGCGGACCTGACCTTTCAC 277

QY 518 ACATTCCTATCCACCTGCGGATGGAGCAACTCAATGACTACTCATTTGGAGACCTTGTCT 577

Db 278 ACTTTTCACTCCCGAGGCTGCTTGGGAGACTCTTGCACACTTTTACGTTGGTATATGAC 337

QY 578 AGGAGAGAGCCC-----CTTGATGATGCTTTAAGACTACAGAGATATGAGAGCC 628

Db 338 GAGAGCGCGCGGATATCAAGATGATGACTTTTCGCGCGCGAGGTCGCAAGCTGCGTACC 397

Search completed: June 18, 2004, 22:56:11
Job time : 829 secs

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Db 398 TGTTCAGAGTCTCTTGGTTTACTACGATTCTTCAAGGCATACTACGCTTCAAGGTCTG 457
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QY 689 ATTATGAGCTCTC-----TTTGTGAGAGATTCGAGCTATCTGTTACGACAGAGT 742
   |||
Db 458 TTCACCTCTGCACTGGGGTTTTCGACGGTCTTGTGGCCAAAGTGGGGCCAGACTCG 517
   |||
QY 743 TACTGGGCTATTGTGTCAGCCAGTTTGAATGGGTCTCTTGTCTCAACAGTGTGATGG 802
   |||
Db 518 ACCCTCGCAACGTCCTCGGCTGGCTTTTGGGTCTGTTCTGGCAGCAGTGGGATGG 577
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QY 803 CTTGCCATGATTTCTCTCATCAAGAGTCTTTGAGAACGCTACGCGAACTCTCTTTT 862
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Db 578 TTGGCTCAGCACTTTTTCATCACCAGGTCTTCCAGGACCGTTTCTGGGGTGTATCTTTT 637
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QY 863 GGTATTTTGTGGCAATTCGTGCTTGGCTTTAGTGTATCATGTTGGTGGAGGAGCAAGC 922
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   |||
QY 923 AACATTATCATACTCTCTCGAATGAGTSCGAGCAACAGTACACACTCTAGACGAAGAC 982
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Db 698 AACACTCACCACGCGCCGCCAACGTCACGGGAGGTCCCGACATTGACCCACCCT 757
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QY 983 ATTGATACTCTCCCATCATCTCTGGAGCAAGGAAATTTTGGCCACCGTTGAGAGCAAG 1042
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Db 758 CTGTTGACCTGGAGTGAGCATGCTGTGGAGATGTTCTCGGATGTCTCCAGATGAGGAGCTG 817
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QY 1043 AGAATTTTGGAGTCTTCAATACAGCACTACATGATTCGTCTTATTTGTTTCATGGCC 1102
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Db 818 ACCCGATGTGGTGGGTTTCATGTTCTTGACCCAGACCTGGTTTACTTCCCATCTC 877
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QY 1103 CGGTACAGTTGGACTTTTGGAAATTTGCTCTTCACATTCAAT----- 1144
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Db 1238 GTTGGATTGAACATATCAGATCGAGCACCACTTGTTCCTTCGATGCTCGCCAACTT 1297
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QY 1541 GTCTCGGTGCTGGTCTCTGTGCGGTGTGCAAGGCGCTCAAGGAAATTTGCTGATGA 1600
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Db 1358 ACCGGTATGATCGAGGGAATCGAGAGGTCTTTTGGCGTCTGAAACGAGGTCTCCAGGCT 1417
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QY 1601 GCTCAATTCGGCTTCACTACTAGAAA 1631
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Db 1418 GCTTCAAGATGGTAAGGCGCAGTAAGAAA 1448
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Maximum Match 100%
Listing first 45 summaries

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6: /cgm2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	7.5	1617	2	US-08-834-655-1
2	153	7.5	1617	3	US-08-834-655-1
3	153	7.5	1617	4	US-09-363-574-1
4	153	7.5	1617	4	US-09-363-574-1
5	153	7.5	1617	4	US-09-330-235-17
6	96	4.7	1686	4	US-09-439-261-6
7	96	4.7	1686	4	US-09-439-261-6
8	96	4.7	1843	4	US-09-439-261-7
9	96	4.7	1843	4	US-09-439-261-7
10	96	4.7	2257	4	US-09-439-261-8
11	96	4.7	2257	4	US-09-439-261-8
12	96	4.7	2540	4	US-09-023-655-295
13	90.2	4.4	1362	4	US-09-769-863-13
14	87.6	4.3	1671	4	US-09-048-888-2
15	87.2	4.3	1684	2	US-08-831-570-1
16	87.2	4.3	1684	2	US-08-831-570-1
17	87.2	4.3	1685	1	US-08-366-779-4
18	87.2	4.3	1685	1	US-08-789-936-4
19	87.2	4.3	1685	4	US-08-934-254-4
20	87.2	4.3	1685	4	US-09-685-775-4
21	80.4	3.9	1478	4	US-09-148-545-63
22	80.4	3.9	2016	4	US-09-148-545-119
23	79.2	3.9	347	4	US-09-702-705-355
24	79.2	3.9	347	4	US-09-736-457-355
25	79.2	3.9	347	4	US-09-614-124B-355
26	79.2	3.9	347	4	US-09-671-325-355
27	79.2	3.9	347	4	US-09-589-184-355

28 79 3.9 449 4 US-09-439-261-38 Sequence 38, Appl
29 79 3.9 449 4 US-09-227-613-37 Sequence 37, Appl
30 79 3.9 473 4 US-09-439-261-37 Sequence 37, Appl
31 79 3.9 473 4 US-09-227-613-36 Sequence 36, Appl
32 79 3.9 655 4 US-09-439-261-3 Sequence 3, Appl
33 79 3.9 655 4 US-09-439-261-3 Sequence 3, Appl
34 79 3.9 864 4 US-09-439-261-12 Sequence 12, Appl
35 79 3.9 864 4 US-09-439-261-12 Sequence 12, Appl
36 79 3.9 1335 4 US-09-439-261-1 Sequence 1, Appl
37 79 3.9 1335 4 US-09-439-261-1 Sequence 1, Appl
38 79 3.9 1928 4 US-09-048-888-4 Sequence 4, Appl
39 62.8 3.1 1320 4 US-09-769-863-28 Sequence 28, Appl
40 51 2.5 1562 1 US-08-330-108-1 Sequence 1, Appl
41 51 2.5 1562 5 PCT-US92-10087-1 Sequence 1, Appl
42 50.8 2.5 19513 4 US-10-204-708-39 Sequence 39, Appl
43 50.6 2.5 593 4 US-09-904-615-59 Sequence 59, Appl
44 50.4 2.5 1413 4 US-09-769-863-19 Sequence 19, Appl
45 49.8 2.4 266 4 US-09-313-294A-3256 Sequence 3256, Ap

ALIGNMENTS

RESULT 1
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MURKERJL, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/POCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEC ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Query Match 7.5%; Score 153; DB 2; Length 1617;
Best Local Similarity 47.9%; Pred. No. 3.7e-34;
Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAGAGAGAGGTGTATGATATAGCGGTTTGGCGACGAC 457
Db 158 GCACCCCTCTTTGATGATCATGACAAAGGTGTACGATGTCGCGAGTTCTGTCCTGAT 217
QY 458 CACCTCGAGGAGCGTAATATAGCACTACTTTGGGGGAGTGCACAGAGTTTTCGCA 517
Db 218 CATCCCGGTGAAGTGTGATTTCCACGCACTGTGGCAAGGAGCGGACATGAGTCTTTGAC 277
QY 518 ACATTCCATCCACCTCGCGCATGGAAGCAACTCAATGACTACTATCTTGGAGACCTTGT 577
Db 278 ACTTTTCAACCGGAGGCTGCTTGGAGACTCTTGCAACTTTTACGTTGTGATATTGAC 337
QY 578 AGGAGAGAGCCC-----CTTGATGAATGCTTAAAGACTACAGAGATATGAGAGCC 628
Db 338 GAGAGGACCGCGATATCAAGAATGATGACTTTTGGCCGAGGTCCGCAAGCTGCTACC 397
QY 629 GAGTTTGTAGAGAGGCTTTCAAGAGTTCGAAGGCTGTTCTGCTTCAGACTGTG 688
Db 398 TTGTTCCAGTCTCTTGGTTACTAGATCTTCCAGGSCNACTAGGCTTCAAGTCTCG 457
QY 689 ATTAATGAGCTCTC-----TTTGTGCGAGCAATTCGACTATCTGTACGACAAGAGT 742
Db 458 TTCAACCTCTGCATCTGGGGTTTGTGCAAGGTCTATTG-GGCCAAGTGGGGCCAGACTCG 517
QY 743 TACTGGCTATTGCTGTAGCCAGTTTGTATGGTCTCTTCGTCGACACTGTGGATGG 802
Db 518 ACCCTCCCAAGTCTCTGGGCTCGCTTTTGGTCTGTTCTGGCAGCACTGGGATGG 577
QY 803 CTTCGCCATGATTTCTTCATCAACAGGTCTTTGAGAACCGTACCGCAACTCTCTCTTT 862
Db 578 TTGGCTCAGACTTTTTCATCACCAGGTCTTCCAGNCCGTTTCTGGGTGATCTTTC 637
QY 863 GGCTATTGTCGCAATTTGGTCTGCTGCTTTAGTATCATGTTGGAGGAGCAAGAC 922
Db 638 GGGCCCTTCTGGAGGTCTGCGAGGGCTTCTGCTCTGTTGGAGGACCAAGCAC 697
QY 923 AACATTCATCATCTGCTCCGAATGAGTGGCAAGACAGATACACACTCTAGAGCAAGAC 982
Db 698 AACACTCACCAGCGCGCCCAAGCTCCAGCGGAGATCCCGACATTGACCCACCGCT 757
QY 983 ATTGATATCTCTCCCATCATCTTCCCTGGAGCAAGAAATTTTGGCCACCGTTGAGCAAG 1042
Db 758 CTGTTGACTCTGGAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCGCCAGATGAGGACTG 817
QY 1043 AGAATTTGGAGTGTCTTCAATATCAGCACTACATGATCTGCTCTATTGTTATGAGCC 1102
Db 818 ACCGCGATGTGGTCGGCTTCTATGCTCTGTAACAGACCTGGTTTACTTCCCATTTCTC 877
QY 1103 OGGTACAGTTGGACTTTTGGAGTTTGTCTCTTCACATTCAAT----- 1144
Db 878 TCGTTTGGCGCTCTCTCTGTTGCTTCCAGTCCCATCTCTTTGTGTCGCTAACGTTGAG 937
QY 1145 -----CTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGGAACAGTTGCT 1192
Db 938 GCCACAAAGCCCTCGGGCGCGGTGTCCTATCTGTTGGTTCGAGCAGCTGTCGCTTGG 997
QY 1193 TTTCACTACGGCTGTTGAGTTGGCTGCTTCCATTTTGGCGGTGTCGCTAAGCT 1252
Db 998 ATGCACTGGACCTGTGTACCTCGCCACCAATGTTCTTGTTCATCAAGGATCCCGTCAACATG 1057
QY 1253 CTTCGGTGGATGATGAACTGAGCTTGTGCGCGTTTGTGTTGGGATTCGTTGTTACG 1312
Db 1058 CTGTTGTTACTTTTGGTGTCCAGCGGTGTGGGAAACTGTTGTTGGCATGTTGTTCTCG 1117
QY 1313 TTGAGTCACAAATGGAAGAGGTTTACAAATGATCG-----AAGGACTTCGTG 1362
Db 1118 CTCAACACACAGGTATGCTGCTGTGATCTCGAAGGAGGAGCGGTGATGATGATTTCTTC 1177
QY 1361 AGAGCCAGGTTATTAACACCCGTAACACCAAGGAGGCTGGTTCAAGATGTTGTTACT 1420
Db 1178 ACBAAGCAGATCATCAGGGTCTGATGTCCACCCGGGTCTATTGTCACACTGGTTACG 1237
QY 1421 GGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAAATGCCCCAGGACACACTAC 1480

Db 1238 GGTGATTGAATATCAGATCGAGCACCATCTGTTCCCTTCGATGCCCTCGCCCAACTTT 1297
QY 1481 CCCAAGATCGCACCTCAGGTCGAGGCTCTTTGCAAGAGACACGGCTCGAGTACGATAAT 1540
Db 1298 TCAAGATCCAGCTGCTGTGCGAGACCTGTGCAAAAGTACAAATGTCGATACCAACC 1357
QY 1541 GTCTCCGTCGTTGCTCTCTGCGGTTGTGAAGGCGCTCAAGGAAATTCCTGATGAA 1600
Db 1358 ACCGTTATGTCGAGGGAACCTGCAAGGCTTTTAGCCCTCTGAAACGAGTCTCCAAGCT 1417
QY 1601 GCGTCAATTCGCTTCAGCTCACTAAGAA 1631
Db 1418 GCCTCAAGATGGTAAGGCGCGTAAAAA 1448

RESULT 2

US-28-834-033A-1
; Sequence 1, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KNUZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: B00

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/POCKET NUMBER: CGAB-300.USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1617 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-834-033A-1

Query Match 7.5%; Score 153; DB 3; Length 1617;

Best Local Similarity 47.9%; Pred. No. 3.7e-34;

Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAGAGAGAGGTGTATGATATAGCGGTTTGGCGACGAC 457

Db 158 GCACCCCTCTTTGATGATCATGACAAAGGTGTACGATGTCGCGAGTTCTGTCCTGAT 217

QY 458 CACCTCGAGGAGCGTAATATAGCACTACTTTGGGGGAGTGCACAGAGCTTTTCGCA 517

Db 218 CATCCCGTGGAACTGATCTCTCAGCACGTTTGGCAAGGACGCACTGACGCTCTTGAC 277

338	DB	GAGAGGACCGCGMATAACAAGATGATGA	CTTTGGCGCGAGGTCCGCAAGCTCGTACC	397
625	QY	GGTTTTCTAGAGAAGGGCTTTTCAAGAGTTC	CAAGCCCTGGTTCTCTGCTTCAGACTCTG	688
398	DB	CTGTTCCAGCTCTTGTTACTACGATTC	TCTTCCAAAGGCATACTAGCGCTTCAAGTCTCG	457
583	QY	ATTAAATCAGCTCTC-----TTTGCTGCGAGCAT	TGGACTATCTGTACGACAGAGT	742
458	DB	TTCAACCTCTGCACTCGGGGTTTGTCACCGT	CATTTGTGCGCAAGTGGGCCAGACCTCG	517
743	QY	TATGGGCTATTTGCTGTGAGCCAGTTTGATGG	GTCTCTTCTGCTTACGACAGAGT	742
518	DB	ACCTCGCCACAGTGTCTCGGCTGGCTTTGG	CTGTCTGTCTGCGACAGTGGCGATGCG	577
803	QY	CTTGCCCATGATTTCTTCTATCAACAGGTCT	TTTGAGAACCGTACCGCGAATCTCTTCTTT	862
578	DB	TTGGCTCACGACTTTTGGCATCACAGGCTC	TCCAGGACCGTTTCTGGGGTGATCTTTTC	637
863	QY	GGCTATTGTTCGCAATTTGGTCTTGGCTTT	AGTGTATCATGCTGTGAGCAAGCAC	922
638	DB	GGCGCTTCTTGGAGGTGTCTGCCAGGGCT	CTCGTCTCTGGTGTGGTAGHACAGCAC	697
923	QY	AACATTCATCATCTGTCTCGAATGAGTGG	CGAGAACAGTACACACTCTAGACGAGAC	982
698	DB	AACACTCACACGCGCGCCCAAGTCCAGGG	CAGGATCCGCACATGCAACCCACCT	757
983	QY	ACTTGATCTCTCCCATCATTTGCTCGAG	GAAGAAATTTTGGCCACCGTGTGAGGACA	1042
758	DB	CTGTTGACTGGAGTGAGATGCGGTGGAG	ATGTTCTCGGATGTCCAGATGAGAGCTG	817
1043	QY	AGAAATTTGGAGTGCTTCAATATACAGCA	CTACATGATTCGCTCTATTGTTCATGCCC	1102
818	DB	ACCGCATGTGTCGCGCTTTCATGGTCT	TGAACAGACCTGGTTTACTTCCCAATCTC	877
1103	QY	CGGTACATTTGGACTTTTGGAAHTTGGT	CTCTTCACTCAAT-----	1144
878	DB	TCGGTTGCCCGCTCTCTCGTGGCTCC	AGTCCCATCTCTTTGTGCTGAACGGTTCAG	937
1145	QY	-----CCTGATTTGAGCACACCAAGGA	TGATAGAGAAAGGAAACAGTTGCT	1192
938	DB	GCCACAAAGCCCTCGGGCGCGTGTGCC	ATCTCGTTGGTTCGAGCAGCTGTGCTTGG	997
1193	QY	TTTCATACGGCTGGTTCAGTGGCTGGT	TCGATTCANATTTTGGCGGTGTGCTAAGCCT	1252
998	DB	ATGCACCTGGACCTGGTACCTCGCCAC	CATGTTCTGTTTCATCAAGGATCCGCTCAA	1057
1253	QY	CTTCGCTGGATGGTAGCACTGTGTGSC	CGGTTTGTGTTGGGATTCGTGTTTACG	1312
1058	DB	CTGGTGTACTTTGGTGTGCGAGCGGT	GTGGGAACTTGTGGCGATCGTGTCTCG	1117
1313	QY	TTGAGTCAATATGAAAGAGGTTTACAAT	GAATTCG-----AAGACTTCGTG	1360
1118	DB	CTCAACACACAACGGTATGCTGTGATCT	CGAAGGAGGAGGGGTGATATGGAATTTCTTC	1177
1361	QY	AGAGCCAGGTTATTTACACCGGTAA	CACCAAGCGAGCTGGTTCAACGATTCGTTCACT	1428
1178	DB	ACGAAGCAGATCATCAGGGTGGTAGT	TCACCCCGGGTCTATTGCGCACTGGTTCACG	1237
1421	QY	GGGGGACTCGACACCCAGATTGACAT	CACCTGTTTCCAAATATGCCAGGCAACACTAC	1480
1238	DB	GGTGGATTGAATATCAGATCGAGCA	CCACTTGTTCCTTCGATGCTCGCCACAACCTT	1297
1481	QY	CCCAAGATCGCACTCAGTTCGAGGCT	TTTTCGAAGAGACACCGCCTCGAGTACGATAAT	1540
1298	DB	TCAAAGAATCCAGCCTGCTGTGAG	ACCTGTGCAAAAAGTACATGTTCGATACCAACC	1357
1541	QY	GTCTCCGCTGTGTGTGCTCTCTGT	CGCGGTTGTGAAGCGGCTCAAGGAAATTTGCTGATGA	1600
1358	DB	ACCGGTAATGATCGAGGAACTG	CAGAGGCTTTAGCCGCTTGACACGAGGCTCTCGAGGCT	1417
1601	QY	CGGTCAATTCGGCTTCACGCTCACT	AAGAAA-----	1631
1418	DB	GCCTCCAAAGATGGTAAAGCGCAGT	AAAAAA-----	1448

RESULT 4
 US-09-363-526-1
 Sequence 1, Application US/09363526
 Patent No. 6410288
 GENERAL INFORMATION:
 APPLICANT: KNU TZON, DEBORAH
 APPLICANT: MURKERUI, PRADIP
 APPLICANT: HUANG, YONG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/363.526
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-201 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1617 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid

	Query Match	7.5%;	Score 153;	DB 4;	Length 1617;
	Best Local Similarity	47.9%;	Pred. No. 3.7e-34;		
	Matches 619;	Conservative 0;	Mismatches 615;	Indels 57;	Gaps 4
Qy	398	GGAGACTGCTGGATGATCGTCAAGAGAGAAAGGTGTATGATATAGCCGTTTTCGGACGAC	457		
Db	158	GCACCCCTCTTGATGATCATGCAACAACAAGGTGTACGAATGCCGCGAGTTCGTCCTGAT	217		
Qy	458	CACCCCTGGAGGACGGTAATTAGCACCTTACTTTGGCGGGATGGCACAGACGTTTTTCGA	517		
Db	218	CATCCCGTGGAAATGTGATCTCTACGCACGTTGGCAAGACGGCACTGACGCTTTTGC	277		
Qy	518	ACATTTCCATCCACTGCGCGATGGAAGCAACTCAATGACTACTACATTGGAGACCTTGCT	577		
Db	278	ACTTTTCACCCCGAGGCTGCTTGGGAGACTCTTGCCAACTTTTACGTTGGTGATATTGC	337		
Qy	578	AGGGAAGAGCC-----CTTGATGAATTGCTTAAAGACTACAGAGATATGAGACC	628		
Db	338	GAGAGCGACCGCGATATCAAGAAATGATGACTTTGCGCGCGAGTCCGCAAGCTCGTACC	397		
Qy	629	GAGTTTGTATAGAGAAGGCGTTTTCAGAGTTTCCAAGGCTCGTCTCTGCTCTTCAGACTCTG	688		
Db	398	TTGTTCACAGCTCTTGTGTTACTACGATTCCTTCCAAGGCATACTACAGCCTTCAAGTCTCG	457		
Qy	689	ATTAATGCAGCTCTC-----TTTGTCTGCGAGCAATTGCGACTATCTGTATGACAAAGAT	742		

458 TTCAACCTCTGATCTGAGTGGTTCGACGGTCAATGTGGCCAGTGGGGCAGACCTCG 517
743 TACTGGGGTATTTGCTGTACAGCAGTGTGAGGTGCTTCTGCTCAACAGTGTGATGG 802
518 ACCCTCGCCAAAGTCTCTCGGCTCGGCTTTTGGGTCTGTCTGAGCAGTGTGGATGG 577
803 CTGCGCCATGATTCCTTCATCAACAGGTCTTTGAGAACCGTACCGGNACTCTCTTT 862
578 TTGGCTCAGACTTTTGATCACCAGGTCTTCCAGGACCGTCTCTGGGGTATCTTTTC 637
863 GCTATTTGTTGGCAATGCTGCTTGGCTTTAGTGTATCATGTTGAGGAGCAGAC 922
638 GCGGCTCTTTGGAGGTCTGCCAGGCTTCTGCTCTGCTGCTGCTGAGCAGAC 597
923 AACATTCATATCTGCTCCGATGAGTGGCAGCAGTACACACTCTAGCAGAC 982
698 AACACTCACCAGCGCCGCCAACGTCACCGCGAGGATCCGACATTCACACCCCT 757
983 ATTGATCTCTCCCATCATTTGCTGAGCAGTACATGATTCGCTCTATTTGCTAGGCC 1042
758 CTGTTGACCTGGAGTACGCTGCTGAGAGTGTCTCGGATGTCCAGATGAGGAGCTG 817
1043 AGAATTTTGGAGTGTCTCAATATCAGCACTACATGATTCGCTCTATTTGCTAGGCC 1102
818 ACCCGCATGTGCTCGCTTTCATGCTCTGAGCAGACCTGCTTTTACTTCCCATCTC 877
1103 CGGTACAGTTGAGTGTGGAGTGTGCTTCTTCACTTCAAT----- 1144
878 TCGTTGCGCGTCTCTCTGCTGCTGCTCCAGTCCATTCTCTTTGCTGCTCAACGGTCA 937
1145 -----CTGATTTGAGCAGCAGGAGGATGATAGAGAGGAGGAGTGTCT 1192
938 GCCCAGACCTCGGGCGGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 997
1193 TTTCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1252
998 ATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
1253 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1312
1058 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1117
1313 TTAGTCTCAATGAGAGGCTTACATGATCG-----AAGACTGCTG 1360
1118 CTCACCAACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
1361 AAGCCAGGTTATACCAACCGCTAACCAAGCAGGCTGCTTCAACGATTTGCTGCT 1420
1178 ACAGAGCAGATCATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1237
1421 GGGGACTCGACACCGATGAGCATACCTGTTTCCAAATGCTGCTGCTGCTGCTGCTG 1480
1238 GGTGATTTGAATATCAGATGAGCAGCCTGTTTCCCTGCTGCTGCTGCTGCTGCTG 1297
1481 CCCAGATCGCAGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1540
1298 TCAGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1357
1541 GTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1600
1358 ACCGATGATCGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1417
1601 GGTCAATTCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1631
1418 GCTTCAAGATGGTAAAGCGCAGTAAAAA 1448

RESULT 5

US-09-330-235-17

; Sequence 17, Application US/09330235

; Patent No. 6459018

; GENERAL INFORMATION:

; APPLICANT: Knutzen, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS

; FILE REFERENCE: MOCO.156.00US

; CURRENT APPLICATION NUMBER: US/09/330,235

; CURRENT FILING DATE: 1999-06-10

; PRIOR APPLICATION NUMBER: 60/889,043

; PRIOR FILING DATE: 1998-06-12

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 1617

; TYPE: DNA

; ORGANISM: Mortierella alpina

US-09-330-235-17

Query Match

Best Local Similarity 7.5%; Score 153; DB 4; Length 1617;

Mismatches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTCTGATGATCTGCAAGAGAGGTGTATGATATTAGCCGTTTSGGAGAC 457
DB 158 GCACCTCTTCTGATGATCATCGAACACAGGTGTACGATGTCCGAGTGTGCTCCCTGAT 217
QY 458 CACCTCTGAGGAGCAGGTAAATTAGCCTACTTTGGCGGGAAGGCACAGACGTTTCGCA 517
DB 218 CATCCCGGTGAGGTGTGATTTCTCAGCAGGTGGCAAGGACGACTGACGCTTTGAC 277
QY 518 ACATTCATTCACCTGCGCATGGAAGCAACTCAATGACTATACATTGGAGACCTTGCT 577
DB 278 ACTTTTCACTCCCGAGGCTGCTTGGGAGACTCTTGCCAACTTTTACGTTGTGATATTGAC 337
QY 578 AGGAGAGACCC-----CTTGATGATTTGCTTAAAGACTACAGAGATATGAGACC 628
DB 338 GAGAGCAGCCGGAATCAAGAAATGATGACTTTGCGGCCGAGTCCGAGCTGCGTACC 397
QY 629 GAGTTTGTAGAGAGGGCTTTTCAAGAGTTCGAAGGCTGTTCTGCTTTCAGACTCTG 688
DB 398 TTGTTTCAAGTCTCTTGTGTTACTACGATTTCTTCAAGGCACTACGCTTCAAGGCTCG 457
QY 689 ATTATGAGCTCTC-----TTTCTGCGAGCATTTGAGCTATCTGTTACGCAAGAT 742
DB 458 TTCAACCTCTGATCTGCGGTGTTGTCAGCAGTCAATTTGCGCAAGTGGGCGCAGACCTCG 517
QY 743 TACTGGCTATGCTGCTCAGCAGTTCAGGCTCTCTGTCACAGTGTGATGG 802
DB 578 ACCCTCGCCAGCTGCTCTGCGCTCGCTTTTGGGTCTGTTCTGCGCAGCAGTGGGATGG 577
QY 803 CTGCGCCATGATTTCTTCTCATCAACAGGTCTTTGAGAACGTCACGCAACTCTTCTTT 862
DB 578 TTGGCTCAGACTTTTTCATCACAGGCTCTTCCAGGACCGTTTCTGGGGTGTATCTTTC 837
QY 863 GCTATTTGTTGGCAATTTGCTGCTGCTTTAGTGTATCATGTTGAGGAGGAGGAGAC 922
DB 638 GCGGCTCTTCTGGGAGGTGCTCGCCAGGCTTCTGCTCTGCTGCTGCTGCTGCTGCTG 697
QY 923 AACATTCATCTACCTGCTCCGANTGAGTCCGAGCAACAGTACACACTCTAGACGAGAC 982
DB 698 AACATTCACACCGCCGCCAACGTCACCGCGAGGATCCCGACATTCGACACCCCT 757
QY 983 ATTGATCTCTCCCATCATTTGCTGAGCAGGAGAAATTTTGGCCACCGTGTGAGAGCAAG 1042
DB 758 CTGTTGACCTGAGTGAAGTCTGTTGGAGTGTCTCGGATGTCCAGATGAGGAGCTG 817
QY 1043 AGAATTTTGGAGTGTCTCAATATCAGCACTACATGATTTCTGCTCTATTGTTGATGGCC 1102
DB 818 ACCCGCATGTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
QY 1103 CGGTACAGTTGAGCTTTTGGAGTGTGCTCTTCTTCACTTCAAT----- 1144
DB 878 TCGTTGCGCGTCTCTCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
QY 1145 -----CTGATTTGAGCAGCAGGAGGATGATAGAGAGGAGGAGTGTCT 1192

Db 938 GCCCAAGGCCCTCGGGGGGGGTGTGTCCTGTCAGAGAGCTGTGCTGGC 997
QY 1193 TTCTACTAGCCTGGTTCAGTTCGGGTGCGTTCCTCAATATTTTGGCGGTGTCGTAAGCCT 1252
Db 998 ATGCACCTGGACCTGGTACCTCGCCACCATTCTCTGTTTCATCAAGGATCCCGTCAACATG 1057
QY 1253 CTTCGCTGGATGTAGCAACTGAGCTGTGCGCGGTGTTGTTGTTGGATTCGTGTTTACG 1312
Db 1058 CTGGTGTACTTTTGGTGTGCGAGCGGTGTGCGAACTTGTGGGATCGTGTCTCG 1117
QY 1313 TTGAGTCACAATGGAAGAGGTTTACAAATGAATCG-----AAGGACTTCGTG 1360
Db 1118 CTCAACCAACAGGTATGCTGTGATCTCGAAGAGGCGGTGATATGGAATTTCTC 1177
QY 1361 AGAGCCAGGTTATTACCAACCGGTAAACCAAGGAGGCTGGTTCAACGATTCGTTCACT 1420
Db 1178 ACGAAGCAGATCATACGGGTGCTGATGTCACCGCGGTCTATTGCGCAACTGGTTCAOG 1237
QY 1421 GGGGGACTCGACCCAGATTGAGCATCACTGTTTCCAAATGCCAGGCAACACTAC 1480
Db 1238 GGTGGATTGAACATATCAGATCGAGCACCCTGTTTCCCTTCGATGCTCCGCCAATTT 1297
QY 1481 CCCAAGATCCACCTCAGGTGCGAGGCTCTTTGCAAGAAGCAGCGCTTCGAGTACGATAT 1540
Db 1298 TCAAGATCCAGCTGCTGCGAGACCTGTGCAAAAGGTACAATGTCCGATACCACACC 1357
QY 1541 GTCCCGTCTGTTGGTCTCTGCGCGGTGTGAGCGCTCAAGGAAATTCGTATGAA 1600
Db 1358 ACCGGTATGATCAGGAGAACTGAGAGGCTTTAGCCGTCTGAACGAGGTCTCCAGGCT 1417
QY 1601 GCGTCAATTCGGTTCACGCTCACTAAGAAA 1631
Db 1418 GCCTCAAGATGGTAAGGCGCAGTAAAAA 1448

RESULT 6

US-09-439-261-6

; Sequence 6, Application US/09439261

; Patent No. 6428990

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pardeep

; APPLICANT: Leonard, Amanda E.

; APPLICANT: Huang, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295-US-P2

; CURRENT APPLICATION NUMBER: US/09/439,261

; CURRENT FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 08/833,610

; PRIOR FILING DATE: 1997-04-11

; PRIOR APPLICATION NUMBER: PCT/US98/07422

; PRIOR FILING DATE: 1998-04-10

; PRIOR APPLICATION NUMBER: US 09/227,613

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 1686

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-261-6

Query Match 4.7%; Score 96; DB 4; Length 1686;

Best Local Similarity 59.5%; Pred. No. 1.4e-17;

Matches 181; Conservative 5; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGATTCTGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350

Db 390 TGGTTTGTGGTTCACACAGATGAATCATGTCATGAGATTGACCGAGGCTTAC 449

QY 1351 --GGACTTCGTGAGAGCCCGAGGTTATTACCAACCGGTAAACCAAGCGAGGCTGGTTCAC 1408

Db 450 CGTGACTGGTTCAGTACCGAGCTGACAGCCACCTGCAACCGTGGAGCAGTCTTCTTCAAC 509

QY 1409 GATTGGTTCCTCGGGGACTCGACCCAGATTGAGCATCACTGTTTCCAAACATGTCGCC 1468
Db 510 GACTGGTTCAGTGAGACACCTTAATCTCCAGATTGAGCACCACCTCTTCCCCCACCATTGCC 569
QY 1469 AGGCACAACCTACCCCAAGATCGCACCTTCAGGTGAGGCTCTTTGCAAGAAGCAGCGCTC 1528
Db 570 CGGCACAACTTACACAAGATCGCCCGCTGGTGAAGTCTCTATGTCGCAAGCATGGCATT 629
QY 1529 GAGTACGATAATGCTCTCCGTCGTTGTCCTCTGTGCGGTTGTGAAGGCGCTCAAGAA 1588
Db 630 GAATACCAAGAGAGCGCTACTGAGGCGCTCTGTCGACATCATCAGGTCCCTGAAGAAG 689
QY 1589 ATTG 1592
Db 690 TCTG 693

RESULT 7

US-09-227-613-6

; Sequence 6, Application US/09227613A

; Patent No. 6432684

; GENERAL INFORMATION:

; APPLICANT: MUKERJI, Pradiip

; APPLICANT: LEONARD, Amanda E.

; APPLICANT: HUANG, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295-US-P1

; CURRENT APPLICATION NUMBER: US/09/227,613A

; CURRENT FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: 08/833,610

; PRIOR FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 1686

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-227-613-6

Query Match

Best Local Similarity 59.5%; Pred. No. 1.4e-17;

Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGATTCTGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350

Db 390 TGGTTTGTGGTTCACACAGATGAATCATGTCATGAGATTGACCGAGGCTTAC 449

QY 1351 --GGACTTCGTGAGAGCCCGAGGTTATTACCAACCGGTAAACCAAGCGAGGCTGGTTCAC 1408

Db 450 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACCGTGGAGCAGTCTTCTTCAAC 509

QY 1409 GATTGGTTCCTCGGGGACTCGACCCAGATTGAGCATCACTGTTTCCAAACATGCCC 1468

Db 510 GACTGGTTCAGTGAGCACCCTTAATCTCCAGATTGAGCACCACCTCTTCCCCCACCATTGCC 569

QY 1469 AGGCACAACCTACCCCAAGATCGCACCTTCAGTCAGGCTCTTTGCAAGAAGCAGCGCTC 1528

Db 570 CGGCACAACTTACACAAGATCGCCCGCTGGTGAAGTCTCTATGTCGCAAGCATGGCATT 629

QY 1529 GAGTACGATAATGTCCTCCGTCGTTGTCCTCTGTGCGGTTGTGAAGGCGCTCAAGAA 1588

Db 630 GAATACCAAGAGAGCGCTACTGAGGCGCTCTGTCGACATCATCAGGTCCCTGAAGAAG 689

QY 1589 ATTG 1592

Db 690 TCTG 693

RESULT 8

US-09-439-261-7

; Sequence 7, Application US/09439261

; Patent No. 6428990

```

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-7

Query Match      4.7%; Score 96; DB 4; Length 1843;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db 547 TGGTTTGTGTGGTCCACACAGATGAATCAGTCGTCATGGAGATTGACCGAGGAGGCTTAC 606
QY 1351 --GGACTTCGTGAGAGCCAGGTTATTACACCCCGTAACACCAAGCGAGGCTGGTTCAAC 1408
Db 607 CGTGACTGGTTTCAGTAGACCACTGACAGCCACTGCAACGTCGAGCAGTCTCTTCTTCAAC 666
QY 1409 GATTGGTTCACTGGGGAGCTGACACCCAGATGAGATGACATCCTGTTTCCAAATGCCC 1468
Db 667 GACTGTTTCAGTGGACACTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 726
QY 1469 AGGCACAACTACCAAGATCGCACCTCAGGTCGAGGCTTTTGCAGAGGACGCGCTC 1528
Db 727 CGGCACAACTTACACAGATCGCCCGCTGCTGAGGCGCTCTGTCGACATCATCAGTCCCTGAGAG 846
QY 1589 ATTG 1592
Db 847 TCTG 850

RESULT 3
US-09-227-613-7
; Sequence 7, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-7
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Query Match      4.7%; Score 96; DB 4; Length 1843;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db 547 TGGTTTGTGTGGTCCACACAGATGAATCAGTCGTCATGGAGATTGACCGAGGAGGCTTAC 606
QY 1351 --GGACTTCGTGAGAGCCAGGTTATTACACCCCGTAACACCAAGCGAGGCTGGTTCAAC 1408
Db 607 CGTGACTGGTTTCAGTAGACCACTGACAGCCACTGCAACGTCGAGCAGTCTCTTCTTCAAC 666
QY 1409 GATTGGTTCACTGGGGAGCTGACACCCAGATGAGATGACATCCTGTTTCCAAATGCCC 1468
Db 667 GACTGTTTCAGTGGACACTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 726
QY 1469 AGGCACAACTACCAAGATCGCACCTCAGGTCGAGGCTTTTGCAGAGGACGCGCTC 1528
Db 727 CGGCACAACTTACACAGATCGCCCGCTGCTGAGGCGCTCTGTCGACATCATCAGTCCCTGAGAG 846
QY 1589 ATTG 1592
Db 847 TCTG 850

RESULT 10
US-09-439-261-8
; Sequence 8, Application US/99439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-8
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Query Match      4.7%; Score 96; DB 4; Length 2257;
Best Local Similarity 59.5%; Pred. No. 1.6e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db 961 TGGTTTGTGTGGTCCACACAGATGAATCAGTCGTCATGGAGATTGACCGAGGAGGCTTAC 1020
QY 1351 --GGACTTCGTGAGAGCCAGGTTATTACACCCCGTAACACCAAGCGAGGCTGGTTCAAC 1408
Db 1021 CGTGACTGGTTTCAGTAGACCACTGACAGCCACTGCAACGTCGAGCAGTCTCTTCTTCAAC 1080
QY 1409 GATTGGTTCACTGGGGAGCTGACACCCAGATGAGATGAGCATTACCTGTTTCCAAATGCCC 1468
Db 1081 GACTGTTTCAGTGGACACTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 1140
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QY 1469 AGGACAACTACCCCAAGATCGCACTCAGTTCAGGCTCTTCCAGAGACGAGGCTC 1528
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Db 1141 CGGCACAACTTACACAGATGCGCCCGCTGGTGAAGTCTCTATGTGCAAGCATGGCAAT 1200
|||
QY 1529 GAGTACGATAATGTCCTCGGTGGTGGTSCCTCTGTCGGGTGTGAAGGCGCTCAAGGAA 1588
|||
Db 1201 GAATACCGAGAGAGCGCTACTGAGGCGCTGCTGCACATCATCAGTCCCTGAGAGAG 1260
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QY 1589 ATTG 1592
|||
Db 1261 TCTG 1264

RESULT 11

US-09-227-613-8
; Sequence 8, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295, US P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-8

Query Match 4.7%; Score 96; DB 4; Length 2257;
Best Local Similarity 59.5%; Pred. No. 1.6e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTGGGATTCGTTTACCTTGAATCAATGGAAGAGGTTTCAATGAATCGAA- 1350
|||
Db 961 TGGTTTGTGGGTCAACACAGATGAATCACATGTCATGAGATTGACAGAGGCGCTAC 1020
|||
QY 1351 --GGACTTCGTGAGAGCCAGGTTATTACCACTGTAACCAAGGAGGCTGTTCAAC 1408
|||
Db 1021 CGTACTGGTTCAGTACGACGCTGACAGCCACCTGCAACGTGAGAGTCTCTTCTCAAC 1380
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QY 1409 GATTGGTTCACTGGGGAGCTGACACCCAGATTGACATCACTGTTTCCAACTATGCC 1468
|||
Db 1081 GACTGGTTCACTGACACCTTAATCTCAGATTGACACCACTCTTCCCACTATGCC 1140
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QY 1469 AGGCACAACTACCCCAAGATCGCACTCAGTGCAGGCTCTTTGCAAGAGACGAGGCTC 1528
|||
Db 1141 CGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCAAT 1200
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QY 1529 GAGTACGATAATGTCCTCGGTGGTGGTCTCTGTCGCGTGTGGAAGGCGCTCAAGAA 1588
|||
Db 1201 GAATACAGAGAGAGCCGCTACTGAGGCGCTGCTGGACATCATAGTCCCTGAGAGAG 1260
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QY 1589 ATTG 1592
|||
Db 1261 TCTG 1264

RESULT 12

US-09-023-655-295
; Sequence 295, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhawer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 295:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT11
; CLONE: 1346478
US-09-023-655-295

Query Match 4.7%; Score 96; DB 4; Length 2540;
Best Local Similarity 59.5%; Pred. No. 1.7e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTGGGATTCGTTTACCTTGAATCAATGGAAGAGGTTTCAATGAATCGAA- 1350
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Db 530 TGGTTTGTGGGTCAACACAGATGAATCACATGTCATGGAGATTGACAGAGGCGCTAC 589
|||
QY 1351 --GGACTTCGTGAGAGCCAGGTTATTACCACTGTAACCAAGGAGGCTGTTCAAC 1408
|||
Db 590 CGTACTGGTTCACTAGCCAGCTGACAGCCACCTGCAACGTGAGAGTCTCTTCTCAAC 649
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QY 1409 GATTGGTTCACTGGGGAGCTGACACCCAGATTGAGCATCACTGTTTCCAACTATGCC 1468
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Db 650 GACTGGTTCACTGAGACACTTAATCTCAGATTGAGCACCACTCTTCCCACTATGCC 709
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QY 1469 AGGCACAACTACCCCAAGATCGCACTCAGTGCAGGCTCTTTGCAAGAGACGAGGCTC 1528
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Db 710 CGGCACAACTTACACAGATCGCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCAAT 769
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QY 1529 GAGTACGATAATGTCCTCGGTGGTGGTCTCTGTCGCGTGTGGAAGGCGCTCAAGAA 1588
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Db 770 GAATACAGAGAGAGCCGCTACTGAGGCGCTGCTGGACATCATAGTCCCTGAGAGAG 829
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QY 1589 ATTG 1592
|||
Db 830 TCTG 833

RESULT 13

US-09-769-863-23
; Sequence 13, Application US/09769863
; Patent No. 6635451

Db 1196 CTGTTTCAGGGGACCTCACTTCCAGATCGAGCACCACCTCTTCCCGAGATGCCGAG 1255
 Qy 1471 GCACAACTACCCCAAGATGCACTCTCAGGTGAGGCTCTTTGCAAGAGCAGGCTCGA 1530
 Db 1256 ACACAACTACAGCCGGGTGGCCCGCTGGTCAAGTGGTGTGCAAGCAGGCTCGAG 1315
 Qy 1531 GTACGATAATGTCCTCGTCTGTTGCTCTGTCGGGTTGTGAAGGCTCAAGGAAT 1590
 Db 1316 CTACGAAGTGAAGCCCTTCCCTCACCGGCTGTGGACATGCTCAGGTCCTCGAAGATC 1375
 Qy 1591 TGCTGA 1596
 Db 1376 TGGTGA 1381

RESULT 15

US-08-831-570-1

; Sequence 1, Application US/08831570

; Patent No. 5959175

; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry L.

; APPLICANT: Nuberger, Andrew N.

; APPLICANT: Beremand, Phillip D.

; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION

; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID

; TITLE OF INVENTION: COMPOSITION

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/831,570

; FILING DATE: 09-APR-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 10545

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 743-4366

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1684 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 43..1387

; US-08-831-570-1

Query Match 4.3%; Score 87.2; DB 2; Length 1684;
 Best Local Similarity 48.4%; Pred. No. 4.9e-15;
 Matches 273; Conservative 0; Mismatches 288; Indels 3; Gaps 2;

Qy 386 CACGACGGCTGGAGATGCTGGATGATCGTCAAGAGAGAGGCTATCATATTTAGCCGT 445
 Db 91 CACGATAACCCGGAGATCTATGGATCTCGATTCAAGGGGAAGCCATATGATCTTCGGAT 150
 Qy 446 TTTCGGGACGACCAACCCCTGGAGGGACGGT---AATTAGCACCTATTTGGCGGGATGGC 502
 Db 151 TGGGTGAAGAGACCATCCAGGTGGCAGCTTTCCTTGAAGAGTCTTGTCTGGTCAAGAGGTA 210

Qy 503 ACAGACGTTTTCGCAACATTCCTCCACTCCCGCATGGAAGCACTCAATGACTACTAC 562
 Db 211 ACTGATGCAATTTGTTGCAATTCCTCCCTCTTACATGGAAGATCTTTGATAAGTTTTTC 270
 Qy 563 ATTGGAGACCTTGTCTAGGGAAGAGCCCTTGATGAATTTGCTTAAAGACTACAGAGATATG 622
 Db 271 ACTGGGTATATCTTAAAGATTACTCTGTTTCTGAGGTTTCTAAAGATTATAGGAAGCTT 330
 Qy 623 AGACCCGAGTTTGTAGAGAAAGGCTTTTCAAGAGTTTCAAGGCTCTGGTTCTCTGCTTCAG 682
 Db 331 GTGTTTGAGTTTCTTAAATGGGTTTGTATCACAAAAGGTCATATTATGTTTGCAACT 390
 Qy 683 ACTCTGATTATAGCAGCTCTCTTTGCTCGGAGCATTCGACTATCTGTTACGACAAGAT 742
 Db 391 TTGTGCTTTATAGCAATGCTGTTTGTCTAAGAGTGTTTATGGGTTTTGTTTGTAGGGT 450
 Qy 743 TACTGGGCTATTGTGCTGTGAGCCAGTTTGTATGGTCTCTTCCTCCAAAGTGTGATGG 802
 Db 451 GTTTTGGTACATTTGTTTCTGGGTTTGTGAGGTTTCTTTGATTTCAGAGTGGTTGG 510
 Qy 803 CTGCCCCATGATTTCTTTCATCAACAGGTCTTTGAGAACCGTACCGGAACTCTCTCTTT 862
 Db 511 ATTGCACATGATGCTGGGCATTATATCGGTAGTGTCTGATTCAAGCTTATAAGTTTATG 570
 Qy 863 GGCTATTGTTTCGCAATTCGCTTGGCTTTTGTGTTTGTATCATGTTGAGGACGAGCAC 922
 Db 571 GGTATTTTGTCTGCAATTTGCTTTTCAGGAATAGTATGTTGTTGGTGGAAATGGACCAT 630
 Qy 923 AACATTTCATCATCTGCTCCGAAT 946
 Db 631 AATGCACATCACATTGCCTGTAAT 654

Search completed: June 19, 2004, 02:39:11
 Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:03:22 ; Search time 59 Seconds
(without alignments)
2313.058 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTPFLNLTGTSKYSV.....AVVKALKEIADIASIRLHAH 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2595	100.0	483	4 AAB46436	Aab46436 C. purpur
2	2595	100.0	483	4 AAB46435	Aab46435 C. purpur
3	1619	62.4	520	4 AAB46440	Aab46440 C. purpur
4	1475	56.8	525	3 AAY51354	Aay51354 Protein b
5	1475	56.8	525	4 AAB46810	Aab46810 P. patens
6	1475	56.8	525	5 ABB98277	Abb98277 Physcomit
7	1475	56.8	525	5 ABB73602	Abb73602 P. patens
8	1475	56.8	525	5 ABB73607	Abb73607 P. patens
9	1475	56.8	525	5 ABB73609	Abb73609 P. patens
10	929	35.8	173	4 AAB46437	Aab46437 C. purpur
11	841.5	32.4	457	2 AAW84137	Aaw84137 A. delta-6
12	841.5	32.4	457	2 AAW95504	Aaw95504 Mortierel
13	841.5	32.4	457	3 AAY56045	Aay56045 Fungal de
14	841.5	32.4	457	3 AAY92599	Aay92599 M. alpina
15	841.5	32.4	457	4 AAB31684	Aab31684 Amino aci
16	841.5	32.4	458	5 ABB96527	Abb96527 M. alpina
17	841.5	32.4	458	5 ABB96509	Abb96509 Human del
18	841.5	32.4	458	5 ABB94707	Abb94707 Human del
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20	839.5	32.4	457	2 AAW85121	Aaw85121 A delta-6
21	799.5	30.8	477	5 ABB98275	Abb98275 Phaeodact
22	799.5	30.8	477	5 ABB73600	Abb73600 P. tricorn
23	798.5	30.8	453	6 AAE31900	Aae31900 Saprolegn
24	790	30.4	459	5 AAE22063	Aae22063 Pythium i
25	705.5	27.2	467	6 ABB99479	Abb99479 Amino aci

26	663.5	25.6	448	3 AAY71551	Aay71551 Florida b
27	649	25.0	355	2 AAW84139	Aaw84139 Desaturas
28	615	23.7	323	5 ABB96515	Abb96515 M. alpina
29	615	23.7	323	5 ABB94698	Abb94698 Human del
30	611.5	23.6	172	4 AAB46438	Aab46438 C. purpur
31	603.5	23.3	458	3 AAY51348	Aay51348 Sphingoli
32	594	22.9	517	3 AAGC7391	Aagc7391 Arabidops
33	587	22.6	449	3 AAY51334	Aay51334 A. thalia
34	587	22.6	449	3 AAG53861	Aag53861 Arabidops
35	584	22.5	449	3 AAG07392	Aag07392 Arabidops
36	583.5	22.5	422	3 AAY96722	Aay96722 E. gracil
37	583	22.5	449	3 AAY51333	Aay51333 B. napus
38	573	22.1	448	2 AAR98455	Aar98455 Borago de
39	573	22.1	448	2 AAW67471	Aaw67471 Borago de
40	573	22.1	448	2 AAW98130	Aaw98130 Borago de
41	572	22.0	448	6 AEG73417	Abg73417 Borago de
42	570	22.0	448	3 AAY51349	Aay51349 Sunflower
43	568	21.9	449	3 AAG29290	Aag29290 Arabidops
44	567	21.8	448	5 AAU79830	Aau79830 Borago of
45	567	21.8	448	6 ABB73095	Abb73095 Borago de

ALIGNMENTS

RESULT 1
AAB46436
ID AAB46436 standard; protein; 483 AA.
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AC AAB46436;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylase/delta6-desaturase SEQ ID NC 4.
XX
KW Delta6-acetylase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.
XX
OS Ceratodon purpureus.
XX
PN W0200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
XX
PR 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymme S, Lee M, Girke T, Sperling P, Zaehring U;
XX
DR WPI; 2001-112150/12.
XX
DR N-PSDB; AAF25730.
XX

XX Nucleic acid encoding delta6-acetylase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.
XX Example 8; Page 49-50; 69pp; German.
XX This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other

CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids
 XX
 XX Sequence 483 AA;

Query Match 100.0%; Score 2595; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 3.8e-266;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVDFLFLGTSWTSKYSVYTHSYAGNYGPTLKHAKVSAQKTAGTQLRQSVQDKKP 60
 DB 1 MALVDFLFLGTSWTSKYSVYTHSYAGNYGPTLKHAKVSAQKTAGTQLRQSVQDKKP 60
 QY 61 GTYSLADVASHDRPGDCMIVKEKYDISRFPADHPGGTIVSTYFGRDGTDVATFHPA 120
 DB 61 GTYSLADVASHDRPGDCMIVKEKYDISRFPADHPGGTIVSTYFGRDGTDVATFHPA 120
 QY 121 AWKQNDYYIGDLAREPDLKDYDMRAEFVREGLFKSSKAWFLQTLINAAALFAAS 180
 DB 121 AWKQNDYYIGDLAREPDLKDYDMRAEFVREGLFKSSKAWFLQTLINAAALFAAS 180
 QY 181 IATICYDKSYWAIWLSASLMGLFVQCGWLADHDFLHQQVFENRTANSFFGYLFGNCVLGF 240
 DB 181 IATICYDKSYWAIWLSASLMGLFVQCGWLADHDFLHQQVFENRTANSFFGYLFGNCVLGF 240
 QY 241 SVSWRTKGNHHTAPNECDQVTPLEDITDPIIAWSKEILLATVESKRLVQLQYOHY 300
 DB 241 SVSWRTKGNHHTAPNECDQVTPLEDITDPIIAWSKEILLATVESKRLVQLQYOHY 300
 QY 301 MILPLLFMARYSWTFGSLLETFNPDLSTTKGLIEKGTVAHYAWFSAWAAHILPGVAKPL 360
 DB 301 MILPLLFMARYSWTFGSLLETFNPDLSTTKGLIEKGTVAHYAWFSAWAAHILPGVAKPL 360
 QY 361 AMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWDFNDFTGGLDT 420
 DB 361 AMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWDFNDFTGGLDT 420
 QY 421 QIEHLEPFTPRHNPYKPIAQVEALCKKHGLEVDNVSVVGASVAVVAKALKEIADEASIRL 480
 DB 421 QIEHLEPFTPRHNPYKPIAQVEALCKKHGLEVDNVSVVGASVAVVAKALKEIADEASIRL 480
 QY 481 HAH 483
 DB 481 HAH 483

RESULT 2
 AAB46435
 ID AAB46435 standard; protein; 483 AA.
 XX
 AC AAB46435;
 XX
 XX
 XX 06-APR-2001 (first entry)
 XX
 DE C. purpureus delta6-acetylase/delta6-desaturase SEQ ID NO 2.
 DE
 DE Delta6-acetylase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic.
 KW
 XX
 XX Ceratodon purpureus.
 OS
 XX
 XX WC200075341-Al.
 PN
 XX
 XX 14-DEC-2000.
 XX
 XX 07-JUN-2000; 20CCWO-EP005274.
 XX

PR 07-JUN-1999; 99DE-01025718.
 PR 22-DEC-1999; 99DE-01062409.
 XX
 XX (BADI } BASF AG.
 XX
 PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
 XX WPI; 2001-112150/12.
 DR N-PSDB; AAF25729.
 XX
 PT Nucleic acid encoding delta6-acetylase or desaturase, useful for
 PT producing plant oils with increased content of unsaturated fatty acids.
 XX
 PS Example 8; Page 44-46; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
 CC polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
 CC activity. The invention also describes (a) amino acid sequences encoded
 CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
 CC more regulatory sequences, (c) a vector containing (I) and EC; (d)
 CC organisms containing (I), EC or the vectors of (c); (e) preparation of
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
 CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
 CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
 CC method (g). (I) are used to produce transgenic plants (or other
 CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids
 XX

SQ Sequence 483 AA;

Query Match 100.0%; Score 2595; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 3.8e-266;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVDFLFLGTSWTSKYSVYTHSYAGNYGPTLKHAKVSAQKTAGTQLRQSVQDKKP 60
 DB 1 MALVDFLFLGTSWTSKYSVYTHSYAGNYGPTLKHAKVSAQKTAGTQLRQSVQDKKP 60
 QY 61 GTYSLADVASHDRPGDCMIVKEKYDISRFPADHPGGTIVSTYFGRDGTDVATFHPA 120
 DB 61 GTYSLADVASHDRPGDCMIVKEKYDISRFPADHPGGTIVSTYFGRDGTDVATFHPA 120
 QY 121 AWKQNDYYIGDLAREPDLKDYDMRAEFVREGLFKSSKAWFLQTLINAAALFAAS 180
 DB 121 AWKQNDYYIGDLAREPDLKDYDMRAEFVREGLFKSSKAWFLQTLINAAALFAAS 180
 QY 181 IATICYDKSYWAIWLSASLMGLFVQCGWLADHDFLHQQVFENRTANSFFGYLFGNCVLGF 240
 DB 181 IATICYDKSYWAIWLSASLMGLFVQCGWLADHDFLHQQVFENRTANSFFGYLFGNCVLGF 240
 QY 241 SVSWRTKGNHHTAPNECDQVTPLEDITDPIIAWSKEILLATVESKRLVQLQYOHY 300
 DB 241 SVSWRTKGNHHTAPNECDQVTPLEDITDPIIAWSKEILLATVESKRLVQLQYOHY 300
 QY 301 MILPLLFMARYSWTFGSLLETFNPDLSTTKGLIEKGTVAHYAWFSAWAAHILPGVAKPL 360
 DB 301 MILPLLFMARYSWTFGSLLETFNPDLSTTKGLIEKGTVAHYAWFSAWAAHILPGVAKPL 360
 QY 361 AMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWDFNDFTGGLDT 420
 DB 361 AMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWDFNDFTGGLDT 420
 QY 421 QIEHLEPFTPRHNPYKPIAQVEALCKKHGLEVDNVSVVGASVAVVAKALKEIADEASIRL 480
 DB 421 QIEHLEPFTPRHNPYKPIAQVEALCKKHGLEVDNVSVVGASVAVVAKALKEIADEASIRL 480
 QY 481 HAH 483

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Db      481 HAH 483
|||||
RESULT 3
AAB46440
ID AAB46440 standard; protein; 520 AA.
AC
XX AAB46440;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 12.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.
XX
OS Ceratodon purpureus.
XX
PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
XX
PS 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASE AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehrerger U;
XX
DR WPI; 2001-112150/12.
XX
DR N-PSDB; AAF25734.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids.
XX
PS Example 7; Page 57-59; 69pp; German.
XX
CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A) or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids
XX
SQ Sequence 520 AA;
Query Match 62.4%; Score 1619; DB 4; Length 520;
Best Local Similarity 61.5%; Pred. No. 2a-162;
Matches 302; Conservative 72; Mismatches 101; Indels 16; Gaps 3;
QY 1 MALVTDLFLNGLCTTWSKSYVYTHSAGNYGPTLKAUKVSAQ-----GKTA 46
DB 25 MFLVSDFLNVLGTLTGQWSLSL-TFAKRLTKTKSHSSDLSVAQKESVARGPWENISQSV 83
QY 47 GQTLQRCSVDKPKPTYSIADVASHDRPGDGMWVKEKYDTSRPAADHPGGTWTSTYFG 106
DB 84 AQPIRRRWQDKPTYSILKDVASHDMPQDCWIIIEKRYDVTFAEQHPGGTINTYFG 143
QY 107 RDGTDVATFPPAAWKOLNDYYIGDLAREPDLKLDYRDMBAEFVEEGLFKSSKAMF 166
DB 144 RDATDVSTFSTHASTSWKILQNFYIGNLVREEPTLELLKEYRELALFLREQLFKSSKSY 203
QY 167 LLQTLNAAALFAASTIATCYDKSYWAIIVLSASLWGLFVQQCGMLAHDFLHQOVFNRTAN 226
DB 204 LFKILNVSIATSIATISLYKSYPAVLLSASLWGLFVQQCGMLSHDFLHQOVFETRWLN 263
QY 227 SFFGYLFGNCVLGFSVSWRTKGNHHTAPNDCDCYTPDLDEIDITLPIIAWSKELLATV 286
DB 264 DVVGWVGNVVLGFSVSWRTKGNHHTAPNDCDCYTPDLDEIDITLPIIAWSKELLATV 323
QY 287 ESKRILRVLOCHYHMLPLIFMARVSYWTEGSLFENPDLSTTKGLEKTVAFHVAWES 346
DB 324 ESKTMLRVLOCHYHMLPLIFMARVSYWTEGSLFENPDLSTTKGLEKTVAFHVAWES 383
QY 347 WAAPHILPGVAKPLAMVATELVAGLLGFFVFTLSHNGKEVYNESKDFVRAQVITTRTK 406
DB 384 SVAFVLLPG-WKPVVWVVSLSMSGLGYGVFLSHNGMEVYNTSKDFVNAQIASTRDIK 442
QY 407 RGWENDWFTGGLDQIEHHEHLEPTMPRHYPKTAPOVEALCKGGLGYDNVSVVGVASVAV 466
DB 443 AGVENDWFTGGLNROIEHHEHLEPTMPRHNLKISPHVETLCKGGLGYEDVSVMSAGTYRVL 502
QY 467 KALKKIADEAS 477
DB 503 KTLKDVADAAS 513
RESULT 4
AAY51354
ID AAY51354 standard; protein; 525 AA.
XX
AC AAY51354;
XX
DT 27-APR-2000 (first entry)
XX
DE Protein b5pp with delta6 fatty acid desaturase activity.
XX
KW Sphingolipid desaturase; sidi; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material.
XX
OS Unidentified.
XX
PN DEL9828850-A1.
XX
PD 30-DEC-1999.
XX
PF 27-JUN-1998; 98DE-01028850.
XX
PR 27-JUN-1998; 98DE-01028850.
XX
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI Heinz E, Zaehrerger U, Schmidt H, Sperling P;
XX
DR WPI; 2000-127549/12.
XX
DE New sphingolipid desaturase that selectively introduces double bond into
PT sphingolipids and capnoids.
XX
PS Disclosure; Fig 16; 62pp; German.
XX
CC This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered delta

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Db 436 VSAQIVSTRDIKGNFNDWFTGGLNRQIEHHLPPTPRNLNKLAPRVEVFCCKGGLVYE 495
QY 455 NVSVVGCASVAVVVKALKEIADEASIRLHA 482
Db 496 DVSIATGCTCKVLKALKEVA-EAAAEQHA 522

RESULT 6
ID ABB98277 standard; protein; 525 AA.
XX
AC ABB98277;
XX
DI 28-MAR-2003 (first entry)
XX
DE Physcomitrella patens desaturase SEQ ID NO 8.
XX
KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW enzyme.
XX
OS Physcomitrella patens.
XX
PN DE10102337-A1.
XX
PD 25-JUL-2002.
XX
PF 19-JAN-2001; 2001DE-01002337.
XX
PR 19-JAN-2001; 2001DE-01002337.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Lerchl J, Renz A, Heinz E, Domerque F, Zaehring U;
XX
WPI; 2002-644810/70.
XX
X-PSDB; ABV74260.
XX
Preparing ester containing polyunsaturated fatty acids, useful e.g. in
animal or human nutrition, by transforming organism with desaturase gene
from Phaseodactylum tricornutum.
XX
Example 5; Page 63-65; 182pp; German.
XX
The invention relates to preparing (M1) fatty acid esters (I) with an
increased content of polyunsaturated fatty acids (II) with at least two
double bonds by introducing into a (i)-producing organism a specific
nucleic acid (A). (M1) is useful for preparing ester containing
polyunsaturated fatty acids. Oils, lipids and (ii) or their fractions,
produced by (M1) are used in animal and human nutrition, cosmetics and
pharmaceuticals, e.g. (ii) are known to reduce levels of cholesterol in
the blood and to protect against heart disease. Cells that express (A)
are also used to identify (ant)agonists of desaturases, e.g. for
modulating the yield and rate of production of particular fine chemicals
in microorganisms (claimed). Also (A) and derived proteins can be used as
markers of specific genomic regions and in evolutionary/protein
structural studies. (M1) is suitable for large scale production (no known
bioengineering method can produce (ii) on a useful scale). The present
sequence is that of a Physcomitrella patens desaturase encoded by a cDNA
used as the (A) component of the invention in producing transgenic (i)-
producing organisms
XX
SQ Sequence 525 AA;

Query Match
Best Local Similarity 56.8%; Score 1475; DB 5; Length 525;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY 1 MALVTDPLNFJGTT---WSKYSVYTHSYAGNYGPTLKHAKVS----- 40
Db 25 MSLSDFDFSYSVSGWSVHSIQPLK-----RLTSKKEVSSEMAVQCISAEVQRNSS 77

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QY 41 -----AOKTGAQTLRQSRVQKPKGTXYSLADVASHDRPGDCWMIYKVKYDISRADD 94
Db 78 TQCTAALAESVVKPTERRSSQWK-STHPLSEAVHNKPSDCWIVVKNKYDVNSFADE 136
QY 95 HPGGTIVISTYFGRDGTDFPATFHPAAWQOLNDYIIGDLAREBPLDELLKQYDRMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVSSHAASTWKILODFYIGDVERVEPTPELLKDFRMRALFL 196
QY 155 REGLFKSSKAWFLLOTLINAALFAASIAITICYDKSWAIVLSASLMGLFYQQCQWLAHDF 214
Db 197 REQLFKSSKLIYVVKLLTWNVAIPAASIAIICWKTISAVLASAKWALCFQCCGWLSHDF 256
QY 215 LHQQVFENRTANSFFCYLFGNCVLFPSVSMWRRTKNIHHTAPNECDQYTPLEDEDITLP 274
Db 257 LHQVFPETRLNEVGVYIGNAVLFSTGWNKEKHLHAAPNECDQYQPIDEDITLP 316
QY 275 LIAWSKEILATVESKEILRVIOYOHVMILPILPMARYSWTFGSLLETFNPDLSITTKGLIE 334
Db 317 LIAWSKDIILATVENKTFLRILOYHILFFMGLFFARGSWLFWSMRYTSTAVLSFVDRLE 376
QY 335 KETVAFHYAFWFAAEHILPGVAKPLAMVAVTELVAGLLIGFVETLSHNGKEVYNESKOF 394
Db 377 KGTVLPHYFVFTACYLLPG-WKPLVMVAVTELMGMLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTYKRWPNDFWFTGGLDQIEHHLPPPTPRNYPKIAPOVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLPPTPRNLNKLAPRVEVFCCKGGLVYE 495
QY 455 NVSVVGCASVAVVVKALKEIADEASIRLHA 482
Db 496 DVSIATGCTCKVLKALKEVA-EAAAEQHA 522

RESULT 7
ABG73602
ID ABG73602 standard; protein; 525 AA.
XX
AC ABG73602;
XX
DT 25-MAR-2003 (first entry)
XX
DE P. patens D6 desaturase SEQ ID 8.
XX
KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific.
XX
OS Physcomitrella patens.
XX
PN DE10102338-A1.
XX
PD 25-JUL-2002.
XX
PF 19-JAN-2001; 2001DE-01002338.
XX
PR 19-JAN-2001; 2001DE-01002338.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX
WPI; 2002-675961/73.
XX
X-PSDB; ABQ76782.
XX
New expression cassette for plant genes, useful for preparing transgenic
plants that have increased production of polyunsaturated fatty acids.
XX
Example 17; Page 67-69; 188pp; German.
XX
This invention describes novel expression cassette (EC) containing at
least one each of plant promoter (P) and structural gene (SG) expressed
in plants, flanked by specific restriction enzyme (RE) recognition sites.
CC

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XX	Physcomitrella patens.
OS	
XX	
PN	DE10102338-A1.
XX	
XX	25-JUL-2002.
XX	
XX	
PF	19-JAN-2002; 2001DE-01002338.
XX	
PR	19-JAN-2002; 2001DE-01002338.
XX	
XX	(BADI) BASF PLANT SCI GMBH.
XX	
PI	Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX	
DR	WEI; 2002-675961/73.
DR	N-PSDB; ABQ76796.

XX New expression cassette for plant genes, useful for preparing transgenic
PT plants that have increased production of polyunsaturated fatty acids.
XX
XX
PS Example 13; Page 155-157; 188pp; German.
XX
XX This invention describes novel expression cassette (EC) containing at
CC least one each of plant promoter (P) and structural gene (SG) expressed
CC in plants flanked by specific restriction enzyme (RE) recognition sites.
CC The EC has the structure (L1-2-SG-L2) n where L1 = is a polylinker
CC (ABQV6798), L2 = any of three synthetic polylinker-terminator-polylinker
CC sequences reproduced (ABQV6799-ABQV6801) or equivalent RE-site-containing
CC sequences and n = 1-3. The invention discloses a vector containing this
CC EC, an organism containing the EC or the vector and a transgenic plant
CC containing a (non-)functional nucleic acid in the vector. Transgenic
CC plants e.g. lineseed can be prepared with improved production of fatty acid
CC esters with an increased content of polyunsaturated fatty acids (PUFA),
CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
CC PUFA are known to reduce levels of cholesterol in the blood and to
CC protect against heart disease. The expression cassettes of the invention
CC provide increased and more efficient production of fine chemicals
CC (especially PUFA), including seed-specific production. This sequence
CC represents a polynucleotide sequence used to illustrate the method of the
CC invention

```

xx
SQ Sequence 525 AA;
Query Match 56.8%; Score 1475; DB 5; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps
6;

Qy 1 MALVTDFLNLGTT---WSKSYVTHSYAGNYGPTLKHAKVY----- 40
. : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 MSLSDFDFSVSVTSVGSWSVHS*QPLK-----RLTSKRVSESAAVCISAEVQRNSS 77

Qy 41 -----AQGKTAGTTLQRQSVQDKPGTYSVLADVASHDRPGDCWMLVKEKYDLSRFADD 94
. : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 TQGTAAALAEVSVKPTRRSSQWK-STHPLSEVAVHNKPSDCWIVKKNKYDVSNFADE 136

Qy 95 HPGGTWISYFGRGGTGVATFHPPAWKQLNDYYIGDLAREPDLKLLKVDKMDMAEFV 154
. : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 HPGGSVISYFGRGGTGVDFSSFFHAASTWKILQDFYIGDVERVEPTPELLKXDFREMLFL 196

Qy 155 REGLFKSSKAWFLQLTLINLAALFAASATIICYDKSYWAIVLSASLMLGFVQQCGWLHDF 214
. : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 REQLFKSSKLDYYMKLNTNVAIFAAISIATICKSTISAVLASACMMALCFQQCGWLHDF 256

Qy 215 LHQOVFNRTANFFGVLFNCVILGFSVSWRRTKNIHHTAPNECDEQVTPLEDIDITLP 274
. : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 LRHQVFPETRLNVEGVGIVNAVILGSTGWKWKKNHLHAAAPNECDQVTPIDEIDITLP 316

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[illegible]

D _b	: : : :	377 KGTWLFHYFWVGACYYLLPG - WKPLVNMVAZELMSGMLLGEVFVLNSNGNEVYSSKEF	435
Q _y	VRAQVIITRTNKRGFNDFWTGGLDTQIEHLFPMPRHNYEKIAPOVEALCKKGLEYD	395	454
D _b	:: :::: : : : : : : : :	436 VSAQIVSTRDIKGNIFNDFMTGGUNRCLIEHLPFTMPRHNLNKIAPRVWFVKKHGLVYE	495
Q _y	NVSVVGASAVVMXALKETADASTRLHA	455	482
D _b	: : : : : : : : : : :	496 DVSATGTCTKVILKALKEVA-EAAAEQHA	522

```

RESULT 9
ABG73609
ID  ABG73609 standard; protein; 525 AA.
XX
XX  AC
ABG73609;
XX
XX  25-MAR-2003 (first entry)
DT
XX
XX
DE  P. patens delta6 desaturase SEQ ID 30.
XX
XX  Promoter; expression cassette; structural gene; plant; transgenic;
KW  linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW  animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW  heart disease; seed-specific.
XX
XX  OS
OS  Physcomitrella patens.
XX
XX  DE10102338-A1.
XX
XX  25-JUL-2002.
XX
XX  19-JAN-2001; 2001DE-01002338.
PF  PE
XX  19-JAN-2001; 2001DE-01002338.
XX  PR
XX  (BADI ) BASF PLANT SCI GMBH.
PA

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Query Match	55.3%	Score 1475;	DB 5;	Length 525;
Best Local Similarity	55.3%	Pred. No. 4e-147;		
Matches 281; Conservative	74;	Mismatches 117;	Indels 35;	Gaps 6;

Example 8; Page 51-52; 69pp; German.

PS This invention describes a novel isolated nucleic acid (I) encoding
 XX polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
 CC activity. The invention also describes (a) amino acid sequences encoded
 CC by (i); (b) an expression cassette (EC) containing (I) linked to one or
 CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
 CC organisms containing (I), EC or the vectors of (c); (e) preparation of
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
 CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
 CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
 CC method (g). (I) are used to produce transgenic plants (or other
 CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (I), resulting in oils with increased
 CC content of saturated fatty acids
 XX
 SQ Sequence 173 AA;

Query Match 35.8%; Score 929; DB 4; Length 173;
 Best Local Similarity 100.0%; Pred. No. 7.1e-90;
 Matches 173; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 251 IHTAPNECEQYTPLEDEDTJPIIAMSKEILATVESKRILRLVLYQHYMILPFLFVAR 310
 DB 1 IHTAPNECEQYTPLEDEDTJPIIAMSKEILATVESKRILRLVLYQHYMILPFLFVAR 60
 QY 311 YSWTGSLLFTNPDLSTTKGLIEKTVAFHAFWSAAAFHILPGVAKPLAWVATELVA 370
 DB 61 YSWTGSLLFTNPDLSTTKGLIEKTVAFHAFWSAAAFHILPGVAKPLAWVATELVA 120
 QY 371 GLLGCVFTLSHNGKEVNESKDFVRAQVITTRNTKRGWENDFWTCGLDTQIE 423
 DB 121 GLLGCVFTLSHNGKEVNESKDFVRAQVITTRNTKRGWENDFWTCGLDTQIE 173

RESULT 11
 AA084137
 ID AA084137 standard; protein; 457 AA.
 AC AA084137;
 DT 15-FEB-1999 (first entry)
 DE A delta-6 desaturase enzyme.
 XX Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition;
 KW inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes;
 KW eczema; platelet aggregation; vasodilation; cholesterol level;
 KW endometriosis; premenstrual syndrome; myalgic encephalomyelitis;
 KW chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome;
 KW hypertension; inflammatory skin disorder.

OS Mortierella alpina.
 XX WO9846763-A1.
 PN 22-OCT-1998.
 XX 10-APR-1998; 98WO-US007126.
 PF 11-APR-1997; 97US-00834655.
 PR (CALJ) CALGENE LLC.
 PA (ABBO) ABBOTT LAB.
 XX Knutson D, Makerji P, Huang Y, Thurmond J, Chaudhary S;
 PI Leonard AE;

WPI; 1988-594582/50.
 N-PSDB; AAV63624.

New isolated fatty acid desaturase enzymes - used for the production of
 PT polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions,
 PT nutritional compositions, cosmetics or animal feed.

Claim 3; Fig 3A-E; 165pp; English.

CC The present sequence represents a Mortierella alpina fatty acid delta-6
 CC desaturase enzyme. The enzyme sequence is used in the methods of the
 CC invention. The specification describes methods for desaturating a fatty
 CC acid and for producing a desaturated fatty acid by expressing increased
 CC levels of a desaturase. The present desaturase is an enzyme which
 CC introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty
 CC acid molecule. The enzyme can be used for desaturating fatty acids. The
 CC enzyme can be used to produce polyunsaturated fatty acids, which can be
 CC used for treating malnutrition, in pharmaceutical compositions, in
 CC cosmetics or in animal feed. The polyunsaturated fatty acids can be used
 CC for treating e.g. restenosis after angioplasty, inflammation, rheumatoid
 CC arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood
 CC pressure. They can also be used to inhibit platelet aggregation, cause
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 CC wall smooth muscle and fibrous tissue, reduce or prevent gastro-
 CC intestinal bleeding and other side effects caused by non-steroidal anti-
 CC inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral
 CC infections, treat AIDS, multiple sclerosis, acute respiratory syndrome,
 CC hypertension and inflammatory skin disorders
 XX
 SQ Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 2; Length 457;
 Best Local Similarity 39.2%; Pred. No. 6.3e-80;
 Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TVSLADV-----ASHDRPGDCWMIKVKYVDCISREADDHPPGGTVISTYFGDGTDFV 113
 DB 9 TTRAEVLNAEALNEGKDAEAPFLMIIDNKYVDVREFVDPHPPGGSVILTHVGKGTDFV 68
 QY 114 ATFHPPAAWKQLNDVYIGDL---AREPELDELLKDYRDMAEFVREGLFKSSKAWFLLQT 170
 DB 69 DTFHPEAAWETLANFVVGDI DESDRDIKNDDFAAEVRLKRLTLFQSLGYDSSKAYAFKV 128
 QY 171 LINAALFAASIA TICY--DKSYNAIVLSASIMGLFVQCGWLAHDHILHQVFENRTANSF 228
 DB 129 SFNLCTIGLSTIVAKWGQSTLTANVLSAALLGLFWQCGWLAHDHILHQVFQDRFWGDL 188
 QY 229 FGVLFNCVLFSGVSWWRKTHHTAPNECDEQYTPLEDEITLPIIAWSK---EILAT 285
 DB 189 FGAFLGGVCGGSSSWKKKXNTHHAAPNVHGE-----DPDIDTHLLTWSHALEMFS 243
 QY 286 VESKRIIRLVQYQHYMIL-----PLLFMARYSWTFGSLFTFNPDLSTTK----- 330
 DB 244 VPDEELTRM--WSRPMVLNQTFYFPILSFARLSWCLQSILFVL--PMGQAHPKSGARVPI 300
 QY 331 GLIEKTVAFHAFWSAAAFHILPGVAKPLAWVATELVAGLLGFVETLSHNGKEVYNE 390
 DB 301 SLVEQLSLAMHWITWYLATMFLFIKDPVNMVFLVPLNSQVCGNLLAIVFSLNNGMVEVSK 360
 QY 391 SK----DFVRAQVITTRNTKRGWENDFWTCGLDTQIEHLLFTPMRPHNPKIAPQVEALC 446
 DB 361 EEAVDMDFTKQIITCRDVHPCGFANWFTGGLNYQIEHLLFSPMRPHNFKIQPAVETLC 420
 QY 447 KKHGLEVDNVSVGASVAVVKALKEIADEAS 477
 DB 421 KKNVRYHTTGMIEGTAEVFSRINEVSKAAS 451

RESULT 12
 AA095504
 ID AA095504 standard; peptide; 457 AA.
 XX

CC essential PAs obtained can be used in nutritional formulations or animal
 CC feed formulations. The long chain PFAs can be used in nutritional
 CC formulations, cosmetic formulations or animal feed formulations. The
 CC products can also be used for producing transgenic animals which can be
 CC used for producing essential PAs which can be used for producing
 CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
 CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
 CC used in cell culture. The animal or milk fat produced can be administered
 CC to treat malnutrition

XX Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 3; Length 457;
 Best Local Similarity 39.2%; Pred. No. 6.3e-80;
 Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSADV-----ASHDRPGDCMIVKEKYVDISRFADDPGGTVISTYFGDGTDFV 113
 DB 9 TTRAEVLNAELNEGKDAEAPFLMIIDNKVYDVREFVDPDFGGSVILTHVGKGTDFV 68

QY 114 ATTHPPAAWKOLNDYIIGDL---AREEPLDELLKYDRMRAEFVRREGLFKSSKAWFLQ 170
 DB 69 DTFHPEAAWETLANFYVGDIDESDRDIKNDPAAEVKRLKTLFQSLGYDSSKAYAFKV 128

QY 171 LNAALFAASIAATICY--DKSYWAILVSASLMGLFVQCGWLAHDFLHQVFENRTANSF 228
 DB 129 SFNLCLWGLSTV-VAKWGQSTLTLANVLSAALLGLFWQCGWLAHDFLHQVDFRWGDL 188

QY 229 FGYLEGNCVLFGRSVWRKTHHTAPNECDQYTPLEDDIDTLPILAMSK---BILAT 285
 DB 189 FGALFGVCGQGFSSWWKDKHHTHAPNVHGE-----DPDIDTHPLTWSEHALEMESD 243

QY 286 VESKRILRVLYQHYMIL-----PLLFMARYSWTFGSLFTFNPLDSTTK----- 330
 DB 244 VPDEELTRM--WSRFVNLQTFVFPILSPARLSWCLQSILFVL-PNGQAHKPSGARVPI 300

QY 331 GLIEKGTVAHYAFWSWAAFHILPGVAKPLAMWVATLVAGLLGLFVFTLSHGKEVYNE 390
 DB 301 SLVEQLSLAHWTWYLAIMFLFTKDPVNLVLYLSQAVCGNLLA-VFSLHNGMPVISK 360

QY 391 SK----DFVAAQVTTTRNTKRGWFMDFGTGLDTQIEHHLFPTWPRNYPKIAPOVEALC 446
 DB 361 EEAVDMDFFTKQITGRDHPGLFANFTGLNLYQIEHLLFSPMRHFNFSKIQPAVETLC 420

QY 447 KHGLEVDNVSVGASVAVVAKLKEIADEAS 477
 DB 421 KTYNRYVHTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 14

AA92599
 ID AA92599 standard; protein; 457 AA.

XX AC AA92599;

XX DT 10-AUG-2000 (first entry)

XX DE M. alpina delta-6 fatty acid desaturase.

XX KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;
 KW transgenic insect cell; polyunsaturated long chain fatty acid;
 KW antiinflammatory; antirheumatic; antiasrhmatic; antipsoriatic;
 KW osteopathic; cycostatic; antidiabetic; dermatological; gynecological;
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
 KW antiaggregant; vasotropic.

XX OS Mortierella alpina.

XX FH Key Location/Qualifiers

FT Misc-difference 172..176

FT /label= histidine box

FT /note= "conserved among membrane-bound desaturases"

FT Misc-difference 209..213

FT /label= histidine box
 FT /note= "conserved among membrane-bound desaturases"
 FT Misc-difference 395..399
 FT /label= histidine box
 FT /note= "conserved among membrane-bound desaturases"

XX WQ200020602-A2.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US022686.

XX 05-OCT-1998; 98US-0103110P.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JM, Das T;

XX WPI: 2000-328935/28.

XX N-PSDB; AAA09430.

XX Novel transgenic insect cells comprising a nucleotide sequences which
 XX encode delta-6-desaturase or delta-12- desaturase, useful for producing
 XX poly-unsaturated long chain fatty acids, e.g. arachidonic acid.

XX Claim 1; Page 145-146; 170pp; English.

XX The fatty acid desaturases are able to catalyze the conversion of oleic
 XX acid to linoleic acid, linoleic acid to gamma-linolenic acid or of alpha-
 XX linolenic acid to stearidonic acid. Transgenic insect cells comprising a
 XX nucleotide sequence which encodes a polypeptide comprising residues 50-
 XX 53, 39-43, 172-176, 204-213, or 390-402 of delta-6 desaturase (AA92599)
 XX or comprising delta-12 desaturase (AA92600) are claimed. Oil and fatty
 XX acids (especially gamma-linolenic acid) isolated from the recombinant
 XX insect cells are also claimed. Production of polyunsaturated long chain
 XX fatty acids (PUFAs) in insect cells has many advantages, as insect cells
 XX have greatly simplified lipid compositions, are not subject to external
 XX variable fluctuations, and can easily be maintained and manipulated. The
 XX oils are used in pharmaceutical compositions, infant formulas, dietary
 XX supplements or substitutes, and cosmetics (all claimed). The PUPA
 XX supplements have antiinflammatory, antirheumatic, antiasrhmatic,
 XX antipsoriatic, osteopathic, cycostatic, antidiabetic, dermatological,
 XX gynecological, anti-HIV, neuroprotective, hypotensive, nephrotropic,
 XX vasodilator, antiaggregant and vasotropic activity

XX Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 3; Length 457;
 Best Local Similarity 39.2%; Pred. No. 6.3e-80;

Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSADV-----ASHDRPGDCMIVKEKYVDISRFADDPGGTVISTYFGDGTDFV 113

DB 9 TTRAEVLNAELNEGKDAEAPFLMIIDNKVYDVREFVDPDFGGSVILTHVGKGTDFV 68

QY 114 ATTHPPAAWKOLNDYIIGDL---AREEPLDELLKYDRMRAEFVRREGLFKSSKAWFLQ 170

DB 69 DTFHPEAAWETLANFYVGDIDESDRDIKNDPAAEVKRLKTLFQSLGYDSSKAYAFKV 128

QY 171 LNAALFAASIAATICY--DKSYWAILVSASLMGLFVQCGWLAHDFLHQVFENRTANSF 228

DB 129 SFNLCLWGLSTV-VAKWGQSTLTLANVLSAALLGLFWQCGWLAHDFLHQVDFRWGDL 188

QY 229 FGYLEGNCVLFGRSVWRKTHHTAPNECDQYTPLEDDIDTLPILAMSK---BILAT 285

DB 189 FGALFGVCGQGFSSWWKDKHHTHAPNVHGE-----DPDIDTHPLTWSEHALEMESD 243

QY 286 VESKRILRVLYQHYMIL-----PLLFMARYSWTFGSLFTFNPLDSTTK----- 330

DB 244 VPDEELTRM--WSRFVNLQTFVFPILSPARLSWCLQSILFVL-PNGQAHKPSGARVPI 300

QY 331 GLIEKGTVAHYAFWSWAAFHILPGVAKPLAMWVATLVAGLLGLFVFTLSHGKEVYNE 390

Db 301 SLVEQLSLAKHTWYLATMELFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNMGPIVSK 360
 QY 391 SK----DEVRAQVITTRNTKRGWENDFTGGLDTQIEHHLFPPTMPRHNYPKIAPOVEALC 446
 Db 361 EEAVDMDFFTKQIITGRDVHGLFANWFTGSLNYQIEHHLFPSPRNPRNFSKIQPAVELC 420
 QY 447 KKHGLEVDNVSVVGASVAVVKALKEIADEAS 477
 Db 421 KKNVRVHTTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 15

AA331684
 ID AAB31684 standard; protein; 457 AA.

AC AAB31684;

XX 30-APR-2001 (first entry)

DE Amino acid sequence of a fungal delta6 desaturase.

XX delta6 desaturase; desaturase gene; elongase gene; fatty acid;

KW eicosanoid; nutrition; infant formula; dietary supplement;

KW dietary substitute; animal feed.

XX Mortierella alpina.

XX WO200104636-A1.

XX 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US019011.

XX 12-JUL-1999; 99US-00351325.

XX (UYOH-) UNIV OHIO.

XX Kopchick JJ, Kelder B;

XX WPI; 2001-182622/18.

DR N-PSDB; AAF25234.

XX New compositions comprising cells that express desaturases and elongases,
 PT for synthesizing essential fatty acids or long-chain polyunsaturated
 PT fatty acids, used in nutritional, cosmetic or animal feed formulations.

XX Disclosure; Fig 9; 93pp; English.

XX The present sequence represents a delta6 desaturase. The desaturase
 CC polynucleotide sequence was used to transfect mammalian cells, to produce
 CC animal cells expressing a desaturase gene and/or an elongase gene.
 CC Compositions comprising cells of the invention are useful for
 CC synthesizing essential fatty acids, their derivatives or downstream
 CC products, as well as altered levels of long-chain polyunsaturated fatty
 CC acids and eicosanoids. The compositions are useful in nutritional
 CC for both humans and animals. The compositions are also useful in cosmetic
 CC or animal feed formulations. Furthermore, the compositions may also be
 CC used as fat free media or as research reagents

XX SQ Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 4; Length 457;
 Best Local Similarity 39.2%; Pred. No. 6.3e-80;
 Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSLADV-----ASHDRPGDCMIVKEKYDISRFADDPHGCTVISTYFGKDGTDVF 113
 Db 9 TFAEVLNAEALNEGKDAEAPFLIIDNKVYDVREFPVDPHGGSVILTHVGKDGTDVF 68

QY 114 ATFFPRAWKQINDYIIGDL---AREEPLDKDYDMRAEFVREGLFKSKAWFLIQT 170

Db 69 DTFPEAEWETIANFYVGDIIDSDRIKNDDFAAEVRKILTLFOSLGYDYSKAYAPKV 128

QY 171 LINAALEAASITATICY--DKSYWAIVLSASLMGLFVQOCGLAHDFLHCQYFENRTANSF 228
 Db 129 SFNLCIWGLSTVIVAKWGQSTLANVLSAALLGLFWOCCGLAHDFLHCQYFQDRFWGDL 188
 QY 229 FGYLEFGNCVLGFSVSWRTKINIIHTAPNECEQYTPLEDEDITLPIIAMS--EILAT 285
 Db 189 FGAEFLGGVCCGFSSSWKKDKHNTTHAAPNVEGE-----DPDIDTHPLLTWSEHALEMFS 243
 QY 286 VESKRILRVLYQYHYMIL-----PLLFMARYSWTFGSLLFTEFNPDLSTTX----- 330
 Db 244 VPDEELTRM--WSRPMVLNQTFWFFPILSPARLSWCLQSILFVL-PNGQAHKPSGARVPI 300
 QY 331 GLIEKGTVAHYAMFSAAFHILPGVAKPLAMVATELVAGLLGFTVTLHGKKEYVNE 390
 Db 301 SLVEQLSLAKHTWYLATMELFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNMGPIVSK 360
 QY 391 SK----DEVRAQVITTRNTKRGWENDFTGGLDTQIEHHLFPPTMPRHNYPKIAPOVEALC 446
 Db 361 EEAVDMDFFTKQIITGRDVHGLFANWFTGSLNYQIEHHLFPSPRNPRNFSKIQPAVELC 420
 QY 447 KKHGLEVDNVSVVGASVAVVKALKEIADEAS 477
 Db 421 KKNVRVHTTGMIEGTAEVFSRLNEVSKAAS 451

Search completed: June 16, 2004, 19:08:06

Job time : 62 secs

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OK protein - protein search, using sw model

Run on: June 16, 2004, 19:05:56 ; Search time 49 Seconds
(without alignments)

2777.015 Million cell updates/sec

Title: US-09-980-468-2

Perfect score: 2595

Sequence: 1 MALVTDLFLNFTGTT...AVVKALKEIADEASIRLHAH 483

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1475	56.8	525	12	US-10-250-821-27
3	1475	56.8	525	12	US-10-250-821-30
4	1475	56.8	525	12	US-10-250-821-4
5	1475	56.8	525	12	US-10-250-821-27
6	1475	56.8	525	12	US-10-250-821-4
7	841.5	32.4	457	14	US-10-278-391-4
8	841.5	32.4	458	14	US-10-191-513A-12
9	841.5	32.4	458	14	US-10-191-513A-41
10	799.5	30.8	477	12	US-10-250-821-4
11	799.5	30.8	477	12	US-10-250-821-4
12	798.5	30.8	453	10	US-09-769-863-14
13	798.5	30.8	453	14	US-10-054-534B-14
14	798.5	30.8	453	14	US-10-431-952-14
15	790	30.4	459	9	US-09-967-477B-8

Sequence 17, Appl
Sequence 11, Appl
Sequence 19828,
Sequence 48669, A
Sequence 13, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 447, App
Sequence 69, Appl
Sequence 22, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 12, Appl
Sequence 447, App
Sequence 179631,
Sequence 52563, A
Sequence 1240, Ap
Sequence 6108, Ap
Sequence 42, Appl
Sequence 9, Appl
Sequence 7, Appl
Sequence 26, Appl
Sequence 8, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 1301, Ap
Sequence 6, Appl

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US-10-702-777-5 14
US-10-231-956A-69 12
US-10-429-160-22 12
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ALIGNMENTS

RESULT 1

US-10-250-821-8

; Sequence 8, Application US/10250821

; Publication No. US20040049805A1

; GENERAL INFORMATION:

; APPLICANT: BASF Plant Science GmbH

; TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes

; TITLE OF INVENTION: in Plant Seeds Using Multiple Expression Constructs

; FILE REFERENCE: 2000-904

; CURRENT APPLICATION NUMBER: US/10/250,821

; CURRENT FILING DATE: 2003-07-07

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Vers. 2.0

; SEQ ID NO 8

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Physcomitrella patens

; US-10-250-821-8

Query Match

Best Local Similarity 56.8%; Score 1475; DB 12; Length 525;

Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY 1 MALVTDLFLNFTGTT---WSKYGVYTHSVAGNVTGPTIKHAKVUS-----40
DB 25 MSLSDFSFYSVSTVGSWSVHSIQPLK-----RLTSKKRVSESAAVQCI SAEVORNS 77
QY 41 -----AQKTAGOTLRSVODKPGTVSLADVASHDRPGCWMTVKVYDISRFAD 94
DB 78 TQGTAAALAESVYKPTRRRSQWKK-STHPLSEVAVHNKPSDCWTVVKNKVDVSNFADE 136
QY 95 HPGGVISTYFGDGTVDVFPATPHPAKQNLNDYVIGDLAREPELDLKYDMDRAEFV 154
DB 137 HPGGVISTYFGDGTVDVFPSSHAATSKWILQDFVIGDVERVEPTPELLKDFREMAFL 136
QY 155 REGLEKSKNAFLQTLNLAALFAASIAITICVDKSYWAIVLSASLMGLFVQCGWJAHDF 214
DB 197 REGLEKSKNLYYWKLLTNVAIFAASIAITICWSKTISAVLASACMMALCFQCGWLSHDF 256

Query Match 56.8%; Score 1475; DB 12; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-146;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
QY 1 MALVDFLNLGTT---WSKSYVTHSYAGNYGPTLKHKAKYS-----40
DB 25 MSLFSDFFSVSVS---VGSWSVHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNS 77
QY 41 -----AQKTAGQTLRQSRVQDKPGCTYSADVASHDRPGDGMVVKYKVDISFADD 94
DB 78 TQCTAEALAEVVKPTRRRESSQWK-SHPLSEVAVHNKPSDCMIVVKNKYVDVSNPADE 136
QY 95 HPGGTVSYVGRDGDVNTATPEPAWKQNDYIGDLAREPDLDELKDYVDMRAEFV 154
DB 137 HPGGSV-STYFGRDGDVFSFPAATWKLQDFYIGDVERVEPTPELLKDFRMRALFL 196
QY 155 REGLFKSSKAWFLQTLINAAALFAASIATICYOKSYNAIVLSASLMGLFVQCGWLAHDF 214
DB 197 REGLFKSSKLIYVVKLLTNVAIFAASIALICWSKTISAVLASACMMALCFQCCWLSHDF 256
QY 215 LHOQFENRTANSEFFGVLCNVLGRSVSWRTKHNHTHTAPNECDQYTPLEDIDITLP 274
DB 257 LHNQFETRWNEVGVVGNVAGFSTGWWKXKHNHHAAPNECDQYQPIDEDIDITLP 316
QY 275 IIAWSKEILATVSKRLRVLYQYOHYMLPFLLEFARYSWTFGSLLLFTFNPDLSTTKLIE 334
DB 317 LIAWSKDILATVENKTLRILOVQHLFPGLLFARGSNLFWSWRYSTAVLSFVDRLE 376
QY 335 KGTVAHYAFWSAAHILFGVAKPLAMVATELVAGLLGFVFTLHNGKEVYNESKDF 394
DB 377 KGTVLFHYFVGTACVLLPG-WKPLVMVAVTELMSCGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITRTKRGWENDWTGGLDTC-EHLEPTEPRHNYPKTAPOVEALCKKHLEYD 454
DB 436 VSAQIVSTRIGKINFDWFTGGLNRQIEHLLFTPMRHNKLAPRVEVFCCKHGLVYE 495
QY 455 NWSVVGASVAVVWKAKEIADEASIRLHA 482
DB 496 DVSATGTCKVLKALKEVA-EAAAEQHA 522

RESULT 7
US-10-278-391-4
; Sequence 4, Application US/10278391
; Publication No. US20030159164A1
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
; KELLER, BRUCE
; HUANG, YUNG-SHENG
; KIRCHNER, STEPHEN J.
; MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/09/087,578

FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CHU-03348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRAND: NO. US20030159164A1 Relevant
TOPOLOGY: NO. US20030159164A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-278-391-4
Query Match 32.4%; Score 841.5; DB 14; Length 457;
Best Local Similarity 39.2%; Pred. No. 2.1e-79;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;
QY 62 TYSLADV-----ASHDRPGDCWMIIVKSKYVDISFADHPGCTVISTYFGRDGDV 113
DB 9 TFRAEVNNALNEGKDAEAPFLMIDNKYVDVREFVPEHPGSLVILTHVGKGDVDF 68
QY 114 ATFFPPAAWKQNDYIGDL---AREEPLDELLKDYDMRAEFVREGLFKSSKAWFLQTL 170
DB 69 DTFPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKRLTLFQSLGYDSSKAYAPKV 128
QY 171 LINAALFAASIATICY--DKSYNAIVLSASLMGLFVQCGWLAHDFLHOQFENRTANSF 228
DB 129 SFNLICGLSTVIYAKNGQSTLANVLSAALLGLFWQCGWLAHDFLHOQFQDFWGD 188
QY 229 FGYLEGNCVLGFSVSWRTKHNHTHTAPNECDQYTPLEDIDITLPIIAWSK---EILAT 285
DB 189 FGALFVGVQCGFSSSWKDKHNTHAAPNVHGE-----DPDIDTHTPLTWSEHALEMPSD 243
QY 286 VESKRIILRVLYQYOHYML-----PLLEFARYSWTFGSLLLFTFNPDLSTTK----- 330
DB 244 VPDEELTRM--WSRFVNLQTFWYFPILSFARLSWCLQSILFVL--PNGQAKKPSGARVPI 300
QY 331 GLIEKGVAFHYAFWSAAHILFGVAKPLAMVATELVAGLLGFVFTLHNGKEVYN 390
DB 301 SLVEQLSLAMHWITLMTFLFKDPVNMVYFLVSQAVCNELAIIVSLHNGMPVLSK 360
QY 391 SK---DFVRAQVITRTKRGWENDWTGGLDTCIEHLLFTPMRHNYPKTAPOVEALC 446
DB 361 EAVDMDFTKQITGRDVHFGLEFANWFTGGLNYQIEHLLFSPMRHNSKIOPAVETLC 420
QY 447 KKHGLEVDNVSVVGASVAVVWKAKEIADEAS 477
DB 421 KKNVVRVHTTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 8
US-10-191-513A-11
; Sequence 11, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10


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; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-11

Query Match      32.4%; Score 841.5; DB 14; Length 458;
Best Local Similarity 39.2%; Pred. No. 2.1e-79;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSLADV-----ASHORPGDCMIVKEKVVYDISRFADDDHGGTGVISTYFGRDGTDFV 113
Db 9 TTRAEVLNAEALNECKDAEAPFLMIIDNKVYDVREFVDPHGGSVILTHVGKGTDFV 68

QY 114 AFPHPPAAKQLNDYIGDL--AREEPDELKDYDRMAEAEVREGLEKSSKAWFLLOT 170
Db 69 DTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLTFLQSLGYDYDSSKAYYAFKV 128

QY 171 LINAALFAASIAIACY--DKSYWAIIVLSASIMGLFVQCCGWLADHDFLHQOVFENRTANSF 228
Db 129 SENLCIWGLSTIVAKWGQSTLANVLAAALGLFWQCCGWLADHDFLHQOVFQDRFWGDL 188

QY 229 FGFLGCVLGSVSWRTKNIHTAPNECDQYTPLEDIDITLPIIAWSK---EILAT 285
Db 189 FGAFGLGVCGQGFSSSWKDKHNTAAAPNVHGE-----DPDIDHTPLLTWSEHALEMFS 243

QY 286 VESKRILRVLYQHYMIL-----PLFMARYSWTFGSLTFENEDLSTTK----- 330
Db 244 VPDEELTRM--NSRFVNLQNTWYFFILSFARLUSWCLQSILFVL--PNGQAHKPSGARVPI 300

QY 331 GLEKGTAVFHYAFWSAAAFHILPGVAKPLAMWVATELVAGLLIGFVFTLSHNGKEYVNE 390
Db 301 SLVEQLSLAMHTWYLATWELFKDPVNMVLYFVLSQAVCGNLLAIVFSLNHNMGMPVISK 360

QY 391 SK----DFVRAQVITTRNTKRGWFDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALC 446
Db 361 EEAVDMDFTKQIITGRDVHPLGFANWFTGGLNYQIEHHLFSPMRHNFSKIQPAVETLC 420

QY 447 KKHGLEVDNVSVVGASVAVVAKKEADEAS 477
Db 421 KKNVRYHTTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 9
US-10-191-513A-4;
; Sequence 41, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardeep
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.B3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-C9-25
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

Query Match      32.4%; Score 841.5; DB 14; Length 458;
Best Local Similarity 39.2%; Pred. No. 2.1e-79;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSLADV-----ASHORPGDCMIVKEKVVYDISRFADDDHGGTGVISTYFGRDGTDFV 113
Db 9 TTRAEVLNAEALNECKDAEAPFLMIIDNKVYDVREFVDPHGGSVILTHVGKGTDFV 68

QY 114 AFPHPPAAKQLNDYIGDL--AREEPDELKDYDRMAEAEVREGLEKSSKAWFLLOT 170
Db 69 DTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLTFLQSLGYDYDSSKAYYAFKV 128

QY 171 LINAALFAASIAIACY--DKSYWAIIVLSASIMGLFVQCCGWLADHDFLHQOVFENRTANSF 228
Db 129 SENLCIWGLSTIVAKWGQSTLANVLAAALGLFWQCCGWLADHDFLHQOVFQDRFWGDL 188

QY 229 FGFLGCVLGSVSWRTKNIHTAPNECDQYTPLEDIDITLPIIAWSK---EILAT 285
Db 189 FGAFGLGVCGQGFSSSWKDKHNTAAAPNVHGE-----DPDIDHTPLLTWSEHALEMFS 243

QY 286 VESKRILRVLYQHYMIL-----PLFMARYSWTFGSLTFENEDLSTTK----- 330
Db 244 VPDEELTRM--NSRFVNLQNTWYFFILSFARLUSWCLQSILFVL--PNGQAHKPSGARVPI 300

QY 331 GLEKGTAVFHYAFWSAAAFHILPGVAKPLAMWVATELVAGLLIGFVFTLSHNGKEYVNE 390
Db 301 SLVEQLSLAMHTWYLATWELFKDPVNMVLYFVLSQAVCGNLLAIVFSLNHNMGMPVISK 360

QY 391 SK----DFVRAQVITTRNTKRGWFDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALC 446
Db 361 EEAVDMDFTKQIITGRDVHPLGFANWFTGGLNYQIEHHLFSPMRHNFSKIQPAVETLC 420

QY 447 KKHGLEVDNVSVVGASVAVVAKKEADEAS 477
Db 421 KKNVRYHTTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 10
US-10-250-821-4
; Sequence 4, Application US/10250821
; Publication No. US20040049805A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes
; TITLE OF INVENTION: in Plant Seeds Using Multiple Expression Constructs
; FILE REFERENCE: 2000-904
; CURRENT APPLICATION NUMBER: US/10/250,821
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 4
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Phaeodactylum tricornutum
US-10-250-821-4

Query Match      30.8%; Score 799.5; DB 12; Length 477;
Best Local Similarity 36.7%; Pred. No. 6e-75;
Matches 177; Conservative 73; Mismatches 161; Indels 71; Gaps 15;

QY 40 SAQKTAGQTLRQSRVQDKKPGTYSLACVASHDRPGDCMIVKEKVVYDISRFADDDHGGT 99
Db 9 ASKGSTAARKI-----SQWEVKTASPEDAMIIHSNKVYDVSNW-HEHFGGA 54
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Search completed: June 16, 2004, 19:09:42
Job time : 51 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 22:56:20 ; Search time 592 Seconds
(without alignments)
3466.013 Million cell updates/sec

Title: US-09-980-468-2

Perfect score: 2595

Sequence: 1 MALVDFLNFGTGWKYSV.....AVVKALKEIADASIRLHAH 483

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 674726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/US0980468/runat_16062004_174741_27165/app_query.fasta_1.647
-DB=N_Geneseq 29Jan04 -QPM=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=ext -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptn -NORM=ext -HEAPSIZ=500 -MINLEN=0 -RCPU=6 -ICPU=3
-USER=US0980468.ecgn_1_1_470 @runat_16062004_174741_27165 -RCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 29Jan04.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2595	100.0	1467	AAF25730	Aaf25730 C. purpur
2	2595	100.0	2040	AAF25729	Aaf25729 C. purpur
3	1619	62.4	2160	AAF25734	Aaf25734 C. purpur
4	1475	56.8	1578	ABV74260	Physcomit
5	1475	56.8	1578	ABQ76782	P. patens
6	1475	56.8	2012	AAF26040	P. patens
7	1475	56.8	2012	ABX13450	P. patens
8	1475	56.8	15430	ABV74274	Plant spe

9	1475	56.8	15430	6	ABQ76796
10	1475	56.8	17752	6	ABV74275
11	1475	56.8	17752	6	ABQ76797
12	925	35.6	520	4	AAF25731
13	841.5	32.4	1374	3	AZ47129
14	841.5	32.4	1374	5	AAF25234
15	841.5	32.4	1617	2	AAV63624
16	841.5	32.4	1617	2	AAV63624
17	841.5	32.4	1617	2	AAV63624
18	799.5	30.8	1434	6	ABV74258
19	799.5	30.8	1434	6	ABQ76780
20	799.5	30.8	1362	7	AD49064
21	790	30.4	1382	6	AD35090
22	705.5	27.2	1404	7	ABV76916
23	663.5	25.6	1471	3	AD01349
24	606.5	23.4	514	4	AAF25732
25	606	23.4	1606	3	AZ44851
26	597	23.0	1650	3	AAC51462
27	597	23.0	1678	3	AZ44833
28	594	22.9	1650	3	AAC33846
29	587	22.6	1350	6	AB212753
30	583	22.5	1594	3	AZ44832
31	577	22.2	1465	3	AAC42244
32	574	22.1	1275	3	AA51233
33	574	22.1	1684	2	AAV34398
34	574	22.1	1684	2	AAV34398
35	574	22.1	1685	2	AAT30395
36	574	22.1	1685	6	ABK49502
37	574	22.1	1685	7	ABX15366
38	567.5	21.9	1764	3	AD31350
39	559	21.5	1463	2	AAV76589
40	555.5	21.4	1972	6	ABK35347
41	555.5	21.4	4203	3	AA93955
42	555.5	21.4	4205	3	AA93952
43	554.5	21.4	2080	4	AAK94270
44	554.5	21.4	2236	4	AAK94234
45	553.5	21.3	1928	7	ABX93652

ALIGNMENTS

RESULT 1	
AAF25730	
ID	AAF25730 standard; DNA; 1467 BP.
XX	
AC	AAF25730;
XX	
DT	06-APR-2001 (first entry)
XX	
DE	C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.
XX	
KW	Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW	transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW	cosmetic; ds.
XX	
OS	Ceratodon purpureus.
XX	
FH	Key Location/Qualifiers
FT	CDS 10..1461
FT	/*tag= a
FT	/product= "delta6-acetylenase/delta6-desaturase"
XX	
FN	WO200075341-A1.
XX	
PD	14-DEC-2000.
XX	
PE	07-JUN-2000; 2000WO-EP005274.
XX	
PR	07-JUN-1999; 99DE-01025718.
PR	22-DEC-1999; 99DE-01062409.
PA	(BADI) BASF AG.
XX	

PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zachringer U;
 XX MPI; 2001-112150/12.
 DR F-PS2B; AA346436.
 XX Nucleic acid encoding delta6-acetylase or desaturase, useful for
 PT producing plant oils with increased content of unsaturated fatty acids.
 XX
 XX
 PS Claim 1a; Page 46-48; 69pp; German.
 XX
 CC This invention describes a novel isolated nucleic acid (I) encoding
 CC polyketides (II) with delta6-acetylase and/or delta6-desaturase
 CC activity. The invention also describes (a) amino acid sequences encoded
 CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
 CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
 CC organisms containing (I); EC or the vectors of (c); (e) preparation of
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
 CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
 CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
 CC method (g). (I) are used to produce transgenic plants (or other
 CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A); or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids
 XX
 SQ Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.2e-284 Length: 1467
 Score: 2595.00 Matches: 483
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-980-468-2 (1-483) x AAF25730 (1-1467)

QY 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThrTrpSerLysTyrSerVal 20
 DB 10 ATGGCCCTCGTTACCGACCTTCTGAACCTTCTGGGCGACGACATGGAGCAAGTACACGGTG 69
 QY 21 TyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLysLysValSer 40
 DB 70 TACACCCATAGCTATGCTGGAAACTATGGCCCTACTTTGAAGCACGCCCAAAAGGTTTCT 129
 QY 41 AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSerValGlnAspLysLysPro 60
 DB 130 GCTCAAGGTAAATCTCGGACACAGACACTGAGACAGATCGGTGAGGACAAAGGCA 189
 QY 61 GlyThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCysTyrMetIle 80
 DB 190 GGCACCTTACTCTGCGCGAATGTGTCTTCACGACGAGGCTTGAGACTGCTGATGATC 249
 QY 81 ValLysGluLysValTyrAspIleSerArgPheAlaAspHisProGlyGlyThrVal 100
 DB 250 GTCAAGAGAGAGGTGATGATATATTAGCCGTTTGGCGACCGACCCCTCGAGGACGGTA 309
 QY 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProAla 120
 DB 310 ATTAGACCTTACTTGGGCGGATGCGACAGAGCGTTTTCGACACATTCCATCCACCTGCC 369
 QY 121 AlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluGluProLeuAsp 140
 DB 370 GCATGAAGCACTCATGACTACTACTACTATGAGACCTTCTAGGAGAGGCCCTTGAT 429
 QY 141 GluLeuLeuLysAspTyrArgAspMetArgAlaGluPheValArgGluGlyLeuPheLys 160
 DB 430 GAATTGCTTAAAGACTACAGATATGAGAGCGGAGTTTGTGTAGAGAGGGCTTTTCAAG 489

QY 161 SerSerLysAlaTyrPheLeuLeuGlnThrLeuIleAsnAlaAlaLeuPheAlaSer 180
 DB 490 AGTTCCAGAGCCCTGGTTCTGCTTCCAGACTGCAATTAATGACGCTCTCTTTGTGGAGC 549
 QY 181 IleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMet 200
 DB 550 ATTGGCACTATCTGTTACCAAGAGGTACTTGGCTATTGTGTGCTGTGACGCACTTGTATG 609
 QY 201 GlyLeuPheValGlnGlnCysGlyTyrLeuAlaHisAspPheLeuHisGlnGlnValPhe 220
 DB 610 GGTCTCTTCGTCACACAGGTGTGATGGCTTGCCCATGATTTCTTCATCAACAGGCTTT 669
 QY 221 GluAsnThrAlaAlaAsnSerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPhe 240
 DB 670 GAGAACCGTACCGCAACTCCCTTTTGGCTATTGTTGGCAATTCGCTGCTGCTGCTTT 729
 QY 241 SerValSerTyrTrpArgThrLysHisAsnIleHisThrAlaProAsnGluCysAsp 260
 DB 730 AGTGTATCATGGTGGAGGACGACACACATTCATCATCTGCTCCGAATGATGCGAC 789
 QY 261 GluGlnTyrThrProLeuAspGluAspIleAspThrLeuProIleIleAlaTyrSerLys 280
 DB 790 GAACAGTACACACCTCTAGACGAGACATGATCTCTCCCATCATTTGCTGCGAGCAAG 849
 QY 281 GluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyr 300
 DB 850 GAATTTTGGCCACCGTTGAGAGCAAGAAATTTGCGAGTGCTTCAATATACGACACTAC 909
 QY 301 MetIleLeuProLeuLeuPheValAlaArgTyrSerTyrThrPheGlySerLeuLeuPhe 320
 DB 910 AGATTCCTGCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGAAGTTTCTCTTC 969
 QY 321 ThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrValAlaPhe 340
 DB 970 ACATTCATCTCTGATTTGAGCACGACCAAGGGATTCATGAGAGAGGAAAGAGTTGCTTT 1029
 QY 341 HisTyrAlaTyrPheSerTyrAlaAlaPheHisIleLeuProGlyValAlaLysProLeu 360
 DB 1030 CACTACGCTGGTTTCAAGTTGGGCTGGCTTCCATATTTTGGCGGCTGTCGCTAAGCTCTT 1089
 QY 361 AlaTyrMetValAlaThrGluLeuValAlaGlyLeuLeuLeuGlyPheValPheThrLeu 380
 DB 1090 GCGTGATGGTAGCACTGAGCTTGTGGCGGTTGTTGTGGATTCGTTTACGTTG 1149
 QY 381 SerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAlaGlnValIle 400
 DB 1150 AGTCAATGGAAGGAGGTTTCAATGAATGGAAGGACTTCGTGAGAGCCGAGGTATT 1209
 QY 401 ThrThrArgAsnThrLysArgGlyTyrPheAsnAspTyrPheThrGlyGlyLeuAspThr 420
 DB 1210 ACCCCCGTAACACCAAGCGGCTGGTTCAACGATTTGTTCACTGGGAGACTCGACACC 1269
 QY 421 GlnIleGluHisLeuPheProThrMetProArgHisAsnTyrProLysIleAlaPro 440
 DB 1270 CAGATTGAGCATCACCTGTTTCCACAAATGCCCGGACCAACTACCCCAAGATCGCACCT 1329
 QY 441 GlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnValSerValGly 460
 DB 1330 CAGGTGCGGCTCTTTGCAAGAGACGCGCTCGAGTACATATGTCTCCGCTGTGGT 1389
 QY 461 AlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeu 480
 DB 1390 GCCTCTGTCGGGTTGTGAAGGCGCTCAAGAAATTTGCTGATCAAGCGTCAATTGGCTT 1449
 QY 481 HisAlaHis 483
 DB 1450 CACGCTCAC 1458
 RESULT 2
 AAF25729 standard; DNA; 2040 BP.
 XX ID AAF25729
 XX AC AAF25729;

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XX DT 06-APR-2001 (first entry)
XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.
XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
XX KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
XX KW cosmetic; ds.
XX OS Ceratodon purpureus.
XX FI Location/Qualifiers
XX FT 176..1627
XX FT /*tag= a
XX FT /product= "delta6-acetylenase/delta6-desaturase"
XX PK WO200075341-A1.
XX PD 14-DEC-2000.
XX PF 07-JUN-2000; 2000WO-EP005274.
XX PR 07-JUN-1999; 99DE-01025718.
XX PR 22-DEC-1999; 99DE-01062409.
XX PA (BADI ) BASF AG.
XX PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX DR MPI; 2001-112150/12.
XX DR P-PSDB; AAB46435.
XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX PT producing plant oils with increased content of unsaturated fatty acids.
XX PS Claim 1a; Page 41-44; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
XX CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
XX CC activity. The invention also describes (a) amino acid sequences encoded
XX CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
XX CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
XX CC organisms containing (I), EC or the vectors of (c); (e) preparation of
XX CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
XX CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
XX CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
XX CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
XX CC method (g). (I) are used to produce transgenic plants (or other
XX CC organisms) that produce oils or triglycerides (TG) with increased content
XX CC of unsaturated fatty acids (A) and to isolate related sequences by
XX CC homology screening. (A), or TG containing them, are useful in human
XX CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
XX CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
XX CC be used to suppress expression of (II), resulting in oils with increased
XX CC content of saturated fatty acids
XX SQ Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,62e-284 Length: 2040
Score: 2595.00 Matches: 483
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-980-468-2 (-483) x AAF25729 (1-2040)

QY 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThrPheSerLysTyrSerVal 20
Db 176 ATGGCCCTCGTTACCGACTTCTCACTTCTGGGCACGACATGGACAGTACAGCGTG 235
QY 21 TyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLysLysValSer 40

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Db 236 TACACCCATAGCTATGCTGGAACTATGGCCCTACTTTTGAACACACCCAAAAGGTTTCT 295
QY 41 AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSerValGlnAspLysLysPro 60
Db 296 GCTCAAGGTAAACTGCGGACACACTGACACAGAGATCGGTGACGACCAAAAGCCCA 355
QY 61 GlyThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCysTyrMetIle 80
Db 356 GGCACCTTACTCTCTGCGCGATGTCTGCTCTACGACAGGCTGGAGACTGCTGGATGATC 415
QY 81 ValLysGluLysValTyrAspIleSerArgPheAlaAspAspHisProGlyGlyThrVal 100
Db 416 GTCAAAGAGAGAGGTGTATGATATTAGCCGTTTTCGGACGACACCTCGAGGGACGGTA 475
QY 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProAla 120
Db 476 ATTAGCACCTACTTTGGGCGGGATGSCACAGACGTTTTCGCAACATTCATCCACTGCGC 535
QY 121 AlaThrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluGluProLeuAsp 140
Db 536 GCATGGAAGCAACTCAATGACTTACTTACATTGGAGACCTTGTAGGACAGAGCCCTTGAT 595
QY 141 GluLeuLeuLysAspTyrArgAspMetArgAlaGluPheValArgGluGlyLeuPheLys 160
Db 596 GAATTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTAGAGAGGGGCTTTTCAAG 655
QY 161 SerSerLysAlaThrPheLeuGlnThrLeuLeuAsnAlaLeuPheAlaAlaSer 180
Db 656 AGTTCCAGGGCTGGTTCCTGCTTCAGACTCTGATTATATGACAGCTCTCTTGTCTGGCAGC 715
QY 181 IleAlaThrIleCysTyrAspLysSerTyrThrAlaIleValLeuSerAlaSerLeuMet 200
Db 716 ATTGCGACTATCTGTACGACAGAGATTACTGGGCTATTGTGCTGTGACGAGTTTGTATG 775
QY 201 GlyLeuPheValGlnGlnCysGlyThrPheAlaHisAspPheLeuHisGlnGlnValPhe 220
Db 776 GGTCTCTTCGTCACACAGTGGATGGCTGCCCCAATGATTTCCCTTCATCAACAGGTCCTT 835
QY 221 GluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPhe 240
Db 836 GAGAACCGTACCGCGAACTCTCTTGGCTATTGTTCGGCAATTGGTGTCTGGCTTT 895
QY 241 SerValSerThrPyrArgThrLysHisAsnIleHisThrAlaProAsnGluCysAsp 260
Db 896 AGTGTATCATGGTGAGGACGAAGCACCAATCATCATATCATCTGCTCCGAATCAGTGGCAG 955
QY 261 GluGlnTyrThrProLeuAspGluAspIleAspThrIleLeuLeuLeuSerLys 280
Db 956 GAACAGTACACACCTCTAGACGAAGACATTGATCTCTCCCCCTCATTCGCTGGAGCAAG 1015
QY 281 GluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyr 300
Db 1016 GAATTTTGGCCACCGTTGAGCAAGAGAAATTTTGGCAGTGTCTCAATATCAGACTAC 1075
QY 301 MetIleLeuProLeuLeuPheMetAlaArgTyrSerTyrThrPheGlySerLeuLeuPhe 320
Db 1076 ATGATTCTGCCTCTATTGTTTCATGSCCGGTACAGTTGGACTTTTGGAAAGTTTGTCTTTC 1135
QY 321 ThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrValAlaPhe 340
Db 1136 ACATTCAATCTGATTTTGGACACCAAGGAGATGTATAGAGAGGGGAACAGTGTCTTTT 1195
QY 341 HisTyrAlaThrPheSerTyrAlaAlaPheHisIleLeuProGlyValAlaLysProLeu 360
Db 1196 CACTACGCTTGTTCAGTTGGGCTGGCTTCCATATTTTGGCGGGTGTGCTTAAGCTCTT 1255
QY 361 AlaThrMetValAlaThrGluLeuValAlaGlyLeuLeuLeuGlyPheValPheThrLeu 380
Db 1256 GCGTGGATGGTAGCACTGAGCTTGTGGCGGTTGTGTGGGATTCGTGTTTACGTTG 1315
QY 381 SerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAlaGlnValIle 400

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Db 1316 AGTCACATGGAAGAGGTTTACATGAATCGAAGACTTCGTGAGAGCCAGGTTATT 1375
 Qy 401 ThrThrArgAsnThrLysArgGlyTyrPheAsnAspTyrPheThrGlyGlyLeuAspThr 420
 Db 1376 ACCACCGTAAACACCAAGCGAGGCTGGTTCAACGATTTGTTCACTGGGGACTCGACACC 1435
 Qy 421 GlnIleGluHisIleuPheProThrMetProArgHisAsnTyrProLysIleLeuAPro 440
 Db 1436 CAGATTGAGCATCACTGTGTTCCAAACATGCCAGGACCAACTACCCCAAGATCGACCT 1495
 Qy 441 GlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnValSerValValGly 460
 Db 1496 CAGGTCAGGCTTTTGCAGACAGACGCTCGAGTACGATTAATGTCCTCGCTGGT 1555
 Qy 461 AlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeu 480
 Db 1556 GCCTGTGCGGGTTGTGAAGCGGCTCAGGAATGCTGATGAAGCGTCAATCGGCTT 1615
 Qy 481 HisAlaHis 483
 Db 1615 CACGCTCAC 1624

RESULT 3

AAF25734

ID AAF25734 standard; DNA; 2160 BP.

XX AAF25734;

DT 06-APR-2001 (first entry)

XX C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.

XX Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic; ds.

XX Ceratodon purpureus.

XX Key Location/Qualifiers
 FT CDS 159..1721
 FT /*tag= a
 FT /product= "delta6-acetylenase/delta6-desaturase"

XX WC200075341-Al.

XX 14-DEC-2000.

XX 07-JUN-2000; 2000WO-EP005274.

XX 07-JUN-1999; 99DB-01025718.

XX 22-DEC-1999; 99DB-01062409.

XX (BAD) BASF AG.

XX Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;

XX WPI; 2001-112150/12.

XX P-PSDB; AAB46440.

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
 FT producing plant oils with increased content of unsaturated fatty acids.

XX Claim 1a; Page 54-57; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
 CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
 CC activity. The invention also describes (a) amino acid sequences encoded
 CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
 CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
 CC organisms containing (I), EC or the vectors of (c); (e) preparation of
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
 CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)

CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
 CC method (g). (I) are used to produce transgenic plants (or other
 CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids

XX SQ Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.39e-173 Length: 2160
 Score: 1619.00 Xatches: 302
 Percent Similarity: 76.17% Conservative: 72
 Best Local Similarity: 61.51% Mismatches: 101
 Query Match: 62.39% Indels: 16
 DB: 4 Gaps: 3

US-09-980-468-2 (1-483) x AAF25734 (1-2160)

Qy 1 YetalaleuValThrAspPheLeuAsnPheLeuGlyThrThrTrpSerLysTyrSerVal 20
 Db 231 ATGCCCTCGTCAGTGACITCTAAATGTCCTGGAAAGACTTTGGGCCAGTGGAGTCTT 290
 Qy 21 TyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLysValSer 40
 Db 291 TCCACT---ACATTGCTTTCAAGAGGCTCACGACTAAGAAACACAGTTCGACATCTCG 347
 Qy 41 AlaGln-----GlyLysThrAla 46
 Db 348 GTGAGGCACAAAAGAAATCGTTCGCGGGGCCAGTTCGAGATATTTCTCAATCGTT 407
 Qy 47 GlyGlnThrLeuArgGlnArgSerValGlnAspLysProGlyThrTyrSerLeuAla 66
 Db 408 GCGCAGCCCATCAGCGGAGGTGGTGCAGGATAAAAGCCGGTTACTTACAGCCTGAAG 467
 Qy 67 AspValAlaSerHisAspArgProGlyAspCysTrpMetIleValLysGluLysValTyr 86
 Db 468 GATGTAGCTTCGCACGATATGCCCCAGGACTGCTGATTATATCAAGAGAGAGTGTAT 527
 Qy 87 AspIleSerArgPheAlaAspAspHisProGlyGlyThrValIleSerThrTyrPheGly 106
 Db 528 GATGTAGCACCTTCGCTGAGCAGCACCTTGAGGSCGGTTCATCAACCTACTTCGA 587
 Qy 107 ArgAspGlyThrAspValPheAlaThrPheHisProProAlaIaThrLysGlnLeuAsn 126
 Db 588 CGAGACGCCACAGATGTTTCTCTACTTCCACGCATCCACCTCATGSAAGATTCTTCAG 647
 Qy 127 AspTyrTyrIleGlyAspLeuAlaArgGluGluProLeuAspGluLeuLysAspTyr 146
 Db 648 AATTCTACATCGGAACCTTGTTAGGAGGAGCCGACTTTGGAGCTGCTGAAGAGGTAC 707
 Qy 147 ArgAspMetArgAlaGluPheValArgGluGlyLeuPheLysSerLysAlaTrpPhe 166
 Db 708 AGAGAGTTGAGAGCCCTTTCTTGAGAGAACAGCTTTCAAGAGTTCCAATCTCTACTAC 767
 Qy 167 LeuLeuGlnThrLeuIleAscAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr 186
 Db 768 CTTTCAAGACTCTCAATAATGTTTCCATTGTTGCCACAAGCATTCGAGATAATCAGTCTG 827
 Qy 187 AspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGln 206
 Db 828 TACAAGCTTTACCGGCGGTTCTGTATACAGCCAGTTTGAAGGCTTGTATTATCAACAG 887
 Qy 207 CysGlyTrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAsnArgThrAlaAsn 226
 Db 888 TCGGATGGTGTCTCAGGATTTCTACACATCAGGTATTTGAGACACGCTGGCTCAAT 947
 Qy 227 SerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpTrpArg 246
 Db 945 GACGTTGTTGCTATGTGTCGCAACGTTGTTCTGGGATTGCTGCTGCTGCTGGAAG 1007

Qy 247 ThrTysHisAsnIleHisThrAlaProAsnGluCysAspGluGlnTyrThrProLeu 266
 Db 1008 ACCAAGCACAACTGCTCAAGTCTCGAATGAATGCGACCAAAAGTACACACCGATT 1067
 Qy 267 AspGluAspIleAspThrLeuProIleIleAlaTrpSerLysGluIleLeuAlaThrVal 286
 Db 1068 GATGAGCATATTGACTCTCCCATCATTCCTGGAGTAAAGATCTCTGGCCACTGTT 1127
 Qy 287 GluSerCysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeuLeu 306
 Db 1128 GAGAGCAGACCATGTTGCGAGTCTTCAGTACACGACCATTTCTTTTGGTCTTTG 1187
 Qy 307 PheMetAlaArgTyrSerTrpThrPheLysSerLeuLeuPheThrPheAsnProAspLeu 326
 Db 1188 ACGTTTCGCGGCGAGTTGGTCTATTGGAGCGCGCTTCACTCTCAGCGCCGAGTTG 1247
 Qy 327 SerThrThrLysGlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSer 346
 Db 1248 ACCCTTGGCAGAGCTTTTGGAGGGGAACGATGGCTTTCAGTACATTTGGTTTAAT 1307
 Qy 347 TrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThr 366
 Db 1308 AGTGTTCGGTTTATCTGCTCCCGGA--TGGAACCAAGTTGATGGATGGTGCAGC 1364
 Qy 367 GluLeuValAlaGlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGlu 386
 Db 1365 GAGCTCATGTCTGCTTCTGCTGGATACCTATTGTACTCAGTCAATGGAATGAG 1424
 Qy 387 ValTyrAsnGluSerLysAspPheValArgAlaGlnValIleThrThrArgAsnThrLys 406
 Db 1425 GTGTACAAATAGCTCAAGAGCTTCGTGAATCCAGATTCAGTACGACGCGGATCAAA 1484
 Qy 407 ArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisLeu 426
 Db 1485 GCAGGGGTGTTATGATGGTTCACCGAGGTCTCAACACACAGATTGAGCATCATCTA 1544
 Qy 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys 446
 Db 1545 TTTTCAACGATGCGCCAGCACAACCTTAATAAATTTCTCTCAGTGGAGACTTTGTGC 1604
 Qy 447 LysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaValVal 466
 Db 1605 AAGAAGCATGACGTGGTCTAGAAAGACGTGAGCATGGCTTCGGGCACCTACCGGTTTIG 1664
 Qy 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477
 Db 1665 AAACACTTAAAGGAGTTCGCGATGCTCTTCA 1697
 RESULT 4
 ID ABV74260 standard; cDNA; 1578 BP.
 XX
 AC ABV74260;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Physcomitrella patens desaturase encoding cDNA SEQ ID NO 7.
 XX
 KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
 KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
 KW gene; ss.
 XX
 OS Physcomitrella patens.
 XX
 FH Key Location/Qualifiers
 CDS 1..1578
 FT /tag=a
 FT /product="desaturase"
 XX
 DE10102337-A1.
 XX
 PD 25-JUL-2002.

XX 19-JAN-2001; 2001DE-01002337.
 XX
 PR 19-JAN-2001; 2001DE-01002337.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Lerchl J, Renz A, Heinz E, Domerque F, Zaehring U;
 XX
 DR WPI; 2002-64481C/70.
 DS P-PSDB; ABB98277.
 XX
 PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
 PT animal or human nutrition, by transforming organism with desaturase gene
 PT from Phaseolactylum tricornutum.
 XX
 PS Example 15; Page 60-63; 182pp; German.
 XX
 CC The invention relates to preparing (M1) fatty acid esters (I) with an
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing
 CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (claimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC bioengineering method can produce (I) on a useful scale). The present
 CC sequence is that of a Physcomitrella patens desaturase encoding cDNA used
 CC as the (A) component of the invention in producing transgenic (I)-
 CC producing organisms
 XX
 SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.9e-157 Length: 1578
 Score: 1475.00 Matches: 281
 Percent Similarity: 69.88% Conservative: 74
 Best Local Similarity: 55.31% Mismatches: 117
 Query Match: 56.84% Indels: 36
 DB: 6 Gaps: 6
 US-09-980-468-2 (1-483) x ABV74260 (1-1578)
 Qy 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
 Db 73 ATGTCCTCTTCAGCGACTTCTCAGTTATGTCCTTCACTGTGGTTCGTCGACCGTA 132
 Qy 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
 Db 133 CACAGTATACAACTTTTGAAG-----CGCTGACGAGTAAGAAG 171
 Qy 38 LysValSer----- 40
 Db 172 CGTGTTCGGAAGCGCTGCGCTGCAATGTATATCAGCTGAGATTTCAGAGAAATTCGAGT 231
 Qy 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
 Db 232 ACCCAGGGAACCTGCGGAGGCACTCCAGAAATCAGTCGTGAGCCACGACGAGAGGTCA 291
 Qy 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
 Db 292 TCTCAGTGGAGAGAG--TCGACACACCCCTATCAGAGTAGCAGTAGTACACAAACGCCA 348
 Qy 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp 94
 Db 349 AGCGATTGCTGATTGTTGTAATAAACAAAGGTGTATGATGTTTCCATTTCGCGACGAG 408
 Qy 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114

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Db 409 CATCCGAGGATCAGTTATTAGTACTATTTTGGACGAGCGCAGAGTTTCTCT 468
Qy 115 ThrPheHisProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
Db 469 AGTTTTCATGAGCTTCTCATGTAATTCITCAAGACTTTTACATTGGTGAAGTGGAG 528
Qy 135 ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal 154
Db 529 AGGGTGGAGCCGACCTCCAGAGCTGCTGGAAGATTTCCGAGAAATGAGAGCTCTTTCCTG 588
Qy 155 ArgGluGlyLeuPheLysSerLysAlaTrpPheLeuLeuGlnThrLeuLeuAsnAla 174
Db 583 AGGGAGCAACTTTTCAAAATTCGAATGTACTATGTTATGAGCTGCTCAGCAATGTT 648
Qy 175 AlaLeuPheAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
Db 649 GCTATTTTGTGGAGCATTCGATAATATGTTGGACGAAGACTATTTCAGCGGTTTG 708
Qy 195 LeuSerAlaSerLeuValGluPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214
Db 709 GCTTCACTGTATGATGAGCTGTGTTTCCACAGTGGGATGGCTATCCCAATATTT 768
Qy 215 LeuHisGlnGluValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
Db 769 CTCACAAATCAGTCTGTTGAGACACGCTGGCTTAATGAGATTCTCGGTATGTGATCGGC 828
Qy 235 AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisThr 254
Db 829 AACGGCGTTCTGGGZFTTATGATCAGGGTGGTGGAGAGGAGCATTAACCTTCATCATGCT 888
Qy 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
Db 889 GCTCCAAATCGAATGCGATCAGACTTACCACCAATGATGAAGATATTGATCTCTCCCC 948
Qy 275 IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
Db 949 CTCATTGCTGGAGCAAGACATCTATGCGCCACAGTTGAGAAATAGACATCTTGGCAATC 1008
Qy 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr 314
Db 1009 CTCCAATACCAAGCATCTGTCTCTTCTATGTTGTTATTTTTCGCCGCTGTATGGCTC 1068
Qy 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
Db 1069 TTGTGAGCTGGAGATPACCTCTACAGCAGTCTCTACCTGTCGACAGTGTGTGGAG 1128
Qy 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 1129 AAGGGAACCTGTTCTGTTTCACTACTTTTGGTTCGTCGGACAGCGTGTATCTTCCTC 1188
Qy 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeu 374
Db 1189 GGT---TGGAGCCATTAGTATGATGGCGGTGACCTAGCTATGTCGCGCATGCTGCTG 1245
Qy 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
Db 1246 GCTTTG---ATTGTACTTACCATATGATGGAGGTTTAAATTCGCTTAAGAAATC 1305
Qy 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 1306 GTGAGTGCACATGCTATCCACGCGGATATCAAGAGAAACATATTCACGACTGGTTC 1365
Qy 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
Db 1366 ACTGTGGCTTTAAACAGGCAATAGAGCATCATCTTTTCCCAACATGCCCAGGCAATAT 1425
Qy 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 1426 TTAACAAATATGACCTAGATGGAGGTGTTCTGTAAAGAAACACGCTCTGGTGAAGAA 1485
Qy 455 AsnValSerValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474

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Db 1486 GAGCTATCTATTCTACGCACTTCGAAAGTTTGAAGCATTGAAGGAAGTCGCG--- 1542
Qy 475 GluAlaSerIleArgLeuHisAla 482
Db 1543 GAGGTCTGCGCAGCAGCAGCATGCT 1566

RESULT 5
ABQ76782
ID ABQ76782 standard; cDNA; 1578 BP.
XX AC ABQ76782;
XX DT 25-MAR-2003 (first entry)
XX DE P. patens D6 desaturase cDNA SEQ ID 7.
KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific; gene; ss.
XX OS Physcomitrella patens.
XX FH Key Location/Qualifiers
XX CDS 1..1578
XX ST /*tag= a
XX FT /product= "D6 desaturase"
XX DE10102338-Al.
XX PN 25-JUL-2002.
XX XX
XX PF 19-JAN-2001; 2001DE-01002338.
XX XX
XX PR 19-JAN-2001; 2001DE-01002338.
XX PA (BADI ) BASF PLANT SCI GMBH.
XX XX
XX PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX WPI; 2002-675961/73.
XX DR P-PSDB; ABG73602.
XX XX
XX ES New expression cassette for plant genes, useful for preparing transgenic
XX plants that have increased production of polyunsaturated fatty acids.
XX Example 17; Page 64-67; 188pp; German.
XX This invention describes novel expression cassette (EC) containing at
XX least one each of plant promoter (P) and structural gene (SG) expressed
XX in plants, flanked by specific restriction enzyme (RE) recognition sites.
XX The EC has the structure (Li-P-SG-L2) n where Li = is a polylinker
XX (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
XX sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
XX sequences and n = 1-3. The invention discloses a vector containing this
XX EC, an organism containing the EC or the vector and a transgenic plant
XX containing a (non-)functional nucleic acid in the vector. Transgenic
XX plants e.g. linseed can be prepared with improved production of fatty acid
XX esters with an increased content of polyunsaturated fatty acids (PUFA),
XX useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
XX PUFA are known to reduce levels of cholesterol in the blood and to
XX protect against heart disease. The expression cassettes of the invention
XX provide increased and more efficient production of fine chemicals
XX (especially PUFA), including seed-specific production. This sequence
XX represents a nucleic acid sequence used to illustrate the method of the
XX invention
XX
XX SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;
Alignment Scores:
Pred. NC.: 4.9e-157 Length: 1578
Score: 1475.00 Matches: 281
Percent Similarity: 69.88% Conservative: 74

```

Best Local Similarity: 55.31% Mismatches: 117
 Query Match: 56.84% Indels: 36
 DB: 6 Gaps: 6

US-09-980-468-2 (1-483) x ABQ67682 (1-1578);

Qy 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TyrSerLys 17
 Db 73 ATGCTCTCTTCAGCGACTTCCTCAGTATGCTGCTTCAACTGTTGGTTCGTGGAGCGTA 132
 Qy 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
 Db 133 CACGATATACAACTTTGAAG-----CGCTCAGCGATGAAG 171
 Qy 38 LysValSer----- 40
 Db 172 CGTGTTCGGAAGCGCTGCGTGCATGTATATCAGCTGAAGTTCAGAGAAATTCGAGT 231
 Qy 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
 Db 232 ACCCAGGGAACCTGGCGGACCTCGCAGATCAGTCGTGAAGCCACCGAGACGAGGTCA 291
 Qy 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
 Db 292 TCTCGTGGAAAGAG---TCGACACCCCTATCAGAAGTAGCGTACCAACAGCCA 348
 Qy 75 GlyAspCysTyrMetIleValLysGlnLysValTyrAspLysArgPheAlaAspAsp 94
 Db 349 AGCGATTGCTGTAATTTGTAAACCAAGGTGATGATGTTTCCAAATTTTGGCGACGAG 408
 Qy 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
 Db 409 CATCCCGGAGGATCAGTATTATAGTACTTATTATTCGACGAGCGGCACAGATGTTTCTCT 468
 Qy 115 ThrPheHisProAlaAlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
 Db 469 AGTTTTCATCGAGCTTCTACATGGAAATTTCTCAGACTTTTACATTTGGTGGCTGGAG 528
 Qy 135 ArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArgAlaSerPheVal 154
 Db 529 AGGTGGAGCGGACTCCAGAGCTGCTGAAGATTTCCGAGAAATGAGAGCTCTTTCTCGT 588
 Qy 155 ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
 Db 589 AGGAGAGACTTTTCAAAAGTTCGAAATTTACTATGTTATGAAGCTGCTCAGCAATGTT 648
 Qy 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTyrAlaIleVal 194
 Db 649 GCTATTTTCTCGCAGCATTTGCATATATATGTTGGACAGACTATTTTCAGCGGTTTG 708
 Qy 195 LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTyrLeuAlaHisAspPhe 214
 Db 709 GCITCAGCTTGATGATGGCTCTGTGTTCCACAGTGGGATGGCTATCCCATGATTTT 768
 Qy 215 LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPheGlyTyrLeuPheGly 234
 Db 769 CTCACCAATCAGGTTGTTGACACACGCTGGCTTATGAAGTTGCGGGTATGATCGGC 828
 Qy 235 AsnCysValLeuGlyPheSerValSerTyrTrpArgThrLysHisAsnIleHisThr 254
 Db 829 AACGCCGTTCTGGGTTTAGTACAGGGTGGTGGAGAGAGCAATACCTTCATCATGCT 888
 Qy 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
 Db 889 GCTCCAAATGAATCCGATCAGACTTACCACCAATTTGATGAAGATATTGATCTCTCCC 948
 Qy 275 IleIleAlaTrpSerLysGluIleAlaThrValGlnSerLysArgIleLeuArgVal 294
 Db 949 CTCATTCCCTGGACAGGACACTACTGCGCCAGCTTGAATAAGACATTTCTCCGAATC 1008
 Qy 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTyrThr 314
 Db 1009 CTCCAATACAGCATCTGTTCTTCATGGTCTGTTATTTTTCGCCCGGTGGTAGTGGCTC 1068

Qy 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
 Db 1069 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCTACCTGTCCACAGGTGTGTGGAG 1128
 Qy 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
 Db 1129 AAGGAACTGTCTCTTCACTACTATTGGTTCGTCGGGACAGCGTGTATCTTCTCCCT 1188
 Qy 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeu 374
 Db 1189 GGT---TGGACCCATTAGTATGGATGGCGGTGATGAGCTCATGTCCCGCATGCTGCTG 1245
 Qy 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
 Db 1246 GGCCTTGTATTGTACTTAGCCACAATGGATGGAGGTTTATAATTCTGCTAAAGAATTC 1305
 Qy 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
 Db 1306 GTGAGTGCACAGATCGTATCCACACGGGATATCAAAAGGAACATATTCACGACTGCTTC 1365
 Qy 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
 Db 1366 ACTGTGGCTTTAACAGGCAATAGAGCATCTCTTTTCCCAACAAATGCCAGGCAAT 1425
 Qy 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
 Db 1426 TTAAACAAATAGCACCTAGAGTGGAGGTGTTCTGTAGAAACACACGGTCTGGTGTACGAA 1485
 Qy 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
 Db 1486 GACGTATCTATTGCTACCGGACTTTCGAAAGGTTTGAAGACATTGAAGGAAGTCGCG--- 1542
 Qy 475 GluAlaSerIleArgLeuHisAla 482
 Db 1543 GAGGCTGGCGAGACGATGCT 1566

RESULT 6
 AAF26C40
 ID AAF26040 standard; cDNA; 2012 BP.
 AC AAF26040;
 XX 23-APR-2001 (first entry)
 XX P. patens delta6-desaturase cDNA.
 DE Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
 XX fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
 XX agricultural chemical; ds.
 XX Physcomitrella patens.
 FH Key Location/Qualifiers
 FT CDS 319..1896
 FT /*tag= a
 FT /product= "delta6-desaturase"
 XX WC200102591-Al.
 XX
 XX 11-JAN-2001.
 XX 04-JUL-2000; 2000WO-EP006223.
 XX 06-JUL-1999; 99US-00347531.
 XX 30-JUN-2000; 2000DE-01030976.
 XX (BADI) BASF AG.
 XX Heinz E, Girke T, Scheffler J, Da Costa E SilvaO;
 XX WPI; 2001-123117/13.
 XX P-PSDE; AAB46810.

XX Production of unsaturated fatty acids, useful e.g. in nutrition,
PT cosmetics or pharmaceuticals, in organisms transformed with
PT Physcomitrella patens de-ta-6-desaturase nucleic acid.
PS
XX Claim 1a; Page 38-41; 49pp; German.
XX This invention describes a novel preparation of unsaturated fatty acids
CC (i) by introducing into an organism at least one isolated nucleic acid
CC (ii) that encodes a polypeptide (iii) with Delta6-desaturase activity.
CC Organisms that contain at least 1 wt.% (i), on total fatty acid content,
CC are then selected. (ii) is selected from: (a) a 2012 bp sequence (S1),
CC defined in the specification, or its equivalents within the degeneracy of
CC the genetic code; or (b) derivatives of the sequence of (a) that encode a
CC 525 amino acid polypeptide (S2), defined in the specification, or a
CC polypeptide with at least 50% homology with (S2) and practically the same
CC enzymatic activity. The invention also describes (i) transgenic organisms
CC that contain (ii); and (2) oils, lipids and fatty acids produced by the
CC new method. The oils, lipids and fatty acids produced by the transformed
CC organisms are used in human or animal nutrition, cosmetics,
CC pharmaceuticals and agricultural chemicals. (iii) can also be used, in
CC vitro, for increasing the (i) content of triglycerides. The transgenic
CC organisms have increased contents of (i), or of (ii)-containing
CC triglycerides, particularly of gamma-linolenic acid
XX
SQ Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7,08e-157 Length: 2012
Score: 1475.00 Matches: 281
Percent Similarity: 69.88% Conservative: 74
Best Local Similarity: 55.33% Mismatches: 117
Query Match: 56.84% Indels: 36
DB: 4 Gaps: 6

US-09-980-468-2 (1-483) x AAF26040 (1-2012)

QY 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
DB 391 ATGTCCTCTTCAGCGACCTTCCTCAGTTATGTCTCACTCTTGGTTCGTGGAGCGTA 450
QY 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
DB 451 CACAGTATACACCTTTGAAG-----CGCTGACGAGTAGAG 489
QY 38 LysValSer----- 40
DB 490 CGTGTTCGGAAGCGCTCCGTCGAATGTATATCATCAGTCAAGTTCAGAGAAATTCGAGT 549
QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
DB 550 ACCGAGGAACTCGGAGGACATCCGAGAAATCATCTGTGAGCCACGAGACGAGGTCA 609
QY 55 ValGlnAspLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
DB 610 TCTCAGTGGGAAG--TCGACACACCCCTATCAGAGTAGCAGTACACACAAAGCCA 666
QY 75 GlyAspCysTyrMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
DB 667 AGCGATTCGTGGATTTGCTAAAAAAACAAGGTGTATGATGTTTCCAAATTTTGGGACGAG 726
QY 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
DB 727 CATCCCGGAGGATCAGTTATAGTACTTATTTGGACGAGACCGCACAGATGTTTCTCT 786
QY 115 ThrPheHisProAlaAlaThrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
DB 787 AGTTTTCATGCAGCTTCTACATCGAAATTCITTCAGAGACTTTTACATTGTTGACGTGGAG 846
QY 135 ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal 154
DB 847 AGGGTGGAGCCGACTCCAGAGCTGCTGAAAGATTTCCGAGAAATGAGAGCTCTTTCTCTG 906

QY 155 ArgGluGlyLeuPheLysSerSerLysAlaTyrPheLeuLeuGlnThrLeuIleAsnAla 174
DB 907 AGGGACAACTTTTCAAAAGTCGAAATGTATCTATGTTATGAGCTGCTCACGAATGTT 966
QY 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTyrAlaIleVal 194
DB 967 GCTATTTTCTCGAGCATTGCAATATATGTTGGAGCAAGACTATTTCAGCGGTTTG 1026
QY 195 LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTyrLeuAlaHisAspPhe 214
DB 1027 GCTTCAGCTTGATGCTCTGTGTTTCCACAGTGCAGTGGTATCCCATGATTTT 1086
QY 215 LeuHisGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
DB 1087 CTCACAATCAGGTGTTGAGACACGCTGCTTAATGAAGTTGTCGGGTATGATCGGC 1146
QY 235 AsnCysValLeuGlyPheSerValSerTyrTyrArgThrLysHisAsnIleHisThr 254
DB 1147 AAGCGCTTCTGGGTTTGTAGTACAGGCTGTGGAAGAGAGACATAACCTTCATGCT 1206
QY 255 AlaProAsnGlnCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
DB 1207 GCTCCAAATGATGCGATCAGACTTACCAACCAATTGATGAAGATATTGATCTCCCC 1266
QY 275 IleIleAlaTyrSerLysGluLeuAlaThrValGluSerLysArgIleLeuArgVal 294
DB 1267 CTCATTGCTGGAGCAAGGACATCTGCGCACAGTTGAGATTAAGACATTTTCGCAATC 1326
QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTyrThr 314
DB 1327 CTCCAATACCAGCATCTGTTCTTCATGGGTCTCTTATTTTTCGCGGTGAGTGGCTC 1386
QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
DB 1387 TTTTGGAGTGGAGATATACCTCTACAGCAGTCTCTCACCTCTCGACAGTGTGTGGAG 1446
QY 335 LysGlyThrValAlaPheHisTyrAlaTyrPheSerTyrAlaAlaPheHisLeuLeuPro 354
DB 1447 AAGGAACTGTTCTGTTTCTACTTCTGTTGTCGGGACAGGTGCTACTTCTCTCCT 1506
QY 355 GlyValAlaLysProLeuAlaTyrMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
DB 1507 GGT---TGGAAAGCCATTAGTATGATGGCGGTGACCTGAGCTCATGTCCGCGCATGCTG 1563
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
DB 1564 GGCCTTTGTATTGTACTCCCAATGGGATGGAGGTTTATTAATTCGTCTAAGAAATTC 1623
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTyrPheAsnAspTyrPhe 414
DB 1624 GTGAGTGCACAGATCGTATCCACCGGATATCAAGGAACATATTCACAGCTGCTTC 1683
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
DB 1684 ACTGTGTGGCTTAAACAGCAATAGAGCATCATCTTTTCCCAACAATGCCAGCGATAAT 1743
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
DB 1744 TTAACAATAATAGACCTAGAGTGGAGGTTCCTGTAAGAAACACCGCTCTGGTGTACGAA 1803
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
DB 1804 GAGGTATCTATTCTACCGGCACCTTCAAGGTTTTCGAAGCAATTGAAGGAAGTCGCG--- 1860
QY 475 GluAlaSerIleArgLeuHisAla 482
DB 1861 GAGGCTCGCGCAGCAGCATGCT 1884
RESULTS
ABX13450
ID ABX13450 standard; DNA; 2012 BP.
XX
AC ABX13450;

04-JUN-2003 (first entry)
P. patens delta6-acyl-lipid desaturase corresponding to Genbank AJ232980.
Expression cassette; transgenic; promoter; LOX5; plant; food production;
animal feed; seed; stress resistance; disease resistance; starch content;
lipid content; dormancy; fibre content; pharmaceutical production;
fine chemical production; sterile plant; vitamin; flavouring; perfume;
dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
Physcomitrella patens.
DE13127862-A1.
12-JEC-2002.
11-JUN-2001; 2001DE-01027882.
11-JUN-2001; 2001DE-01027882.
(BADI) BASF PLANT SCI GMBH.
Bischoff P, Feussner I, Loyall LP;
WPI; 2003-279966/28.
Cassette for expressing transgene, useful e.g. in production of
pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
of Arabidopsis, provides cotyledon-specific expression.
Claim 5; Page: 28pp; German.
This invention describes a novel cassette for the transgenic expression
of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
thaliana or deletion variants of the LOX5 promoter which are functionally
linked to the nucleic acid of the invention. The cassette is used to
prepare transgenic organisms, especially plants, for production of foods,
animal feeds, seeds (including those with increased resistance to stress
and disease, altered starch/lipid contents or dormancy, or altered fibre
content), pharmaceuticals (especially antibodies, vaccines, enzymes and
pharmaceutical proteins) and fine chemicals (especially enzymes,
vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
perfumes and dyes), also to produce sterile plants. The LOX5 promoter
provides strong and specific expression in cotyledons and/or other early
embryonic tissue, so can degrade, or protect against, stress factors to
which these tissues are particularly sensitive. Since cotyledons are the
main storage organs of seeds, expressing transgenes in them produces
targeted increases/modifications in nutritional value. Expression in the
cotyledons is homogeneous, there are no side effects on other plant
organs (pollen) and the promoter is functional in a wide variety of
plants (ornamentals or crops). This sequence represents a nucleic acid
sequence associated with the Arabidopsis thaliana LOX gene described in
the disclosure of the invention

Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7,08e-157	Length:	2012
Score:	1475.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	7	Gaps:	6

US-09-380-468-2 (1-483) x ABX13450 (1-2012)

1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
391 ATGTCCTCTTCACGGACTCTTCAGTATGATGCTTCACACTGGTTCGGAGCGTA 450
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

18 TrpSerValThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal	194
DB	13961	GCTATTTTTGGCTCGGAGCATTGCAATAATATGTTGGAGCAAGACTATTTCAGCGGTTTG	14020
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe	214
DB	14021	GCTTCAGCTGTGATGATGCTCTGTGTTCCTAACACAGTCGGATGCTATCCCATGATTTT	14080
QY	215	LeuHisGlnGluValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234
DB	14081	CTCCAAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTGTCCGGTATGTGATCGGC	14140
QY	235	AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisThr	254
DB	14141	AACCGCGTCTCGGGTTTAACTACAGGGTGTGGAAGGAGACATAACCTTCATCATGCT	14200
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro	274
DB	14201	GCTCCAAATGMAATGCGATCAGACTTACCACCAATATGATGAAGATATTGATACTCTCCCC	14260
QY	275	IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal	294
DB	14261	CTCATTCCTCGGACGAGACATACCTGGCCACAGTTGGAATTAAGACATCTCTCGCAATC	14320
QY	295	LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr	314
DB	14321	CYCCAAATACAGCATCTGTTCTTCATGGGTCTGTATTATTTTCGCCGGGTAGTTGGTCT	14380
QY	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334
DB	14381	TTTTGGAGCTGGAGATATACCTTCACGACAGTGTCTCACCTGTGCGACAGGTTGTGGAS	14440
QY	335	LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro	354
DB	14441	AAGGAACTGTGTTCTGTTCACACTCTTTTGTTCTCGTGGGACAGCGTGCTATCTTCCTCCCT	14500
QY	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu	374
DB	14501	GST--TGGAGCCATTATGATGGATGGCGGTGACTGAGCTCATCTCCGCGATGCTGCTG	14557
QY	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe	394
DB	14558	GGCTTTGTATTGTACTTAGCCACAAATGGGATGGAGGTTTATTAATCGTCTTAAGAAATC	14617
QY	395	ValArgAlaAlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe	414
DB	14618	GTGAGTGCCACAGATCGTATCCACACGGGTATCAAAGGAACATATTCAACGACTGGTTC	14677
QY	415	ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn	434
DB	14678	ACTGGTGGCGTTTAAACAGGCAAAATAGACATCATCTTTTCCCAACAATGCCAGGCATAA	14737
QY	435	TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGlnTyrAsp	454
DB	14738	TTAAACAAATAGCACCCTAGAGTGGAGGTGTCTGTAGAAACACCGGTCTGGTGTACGA	14797
QY	455	AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp	474
DB	14798	GAGGTATCTATTGCTACCGGCACCTGCCAAGGTTTGAAGGATTTGAAGGAAGTCGCG--	14854
QY	475	GluAlaSerIleArgLeuHisAla	482
DB	14855	GAGGCTGGCGCAGACAGCATGCT	14878

DE	XX	pB-DHGLA encoding P. patens delta6 elongase and delta6 desaturase.	
KW	XX	Promoter; expression cassette; structural gene; plant; transgenic;	
KW	XX	linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;	
KW	XX	animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;	
KW	XX	heart disease; seed-specific; gene; ds.	
XX	XX		
XX	XX	Physcomitrella patens.	
OS	XX	Synthetic.	
XX	XX		
FH	XX	Key	Location/Qualifiers
FT	XX	CDS	11543..12415
FT	XX		/*tag= a
FT	XX		/product= "delta6 elongase"
FT	XX	CDS	13313..14890
FT	XX		/*tag= b
FT	XX		/product= "delta6 desaturase"
XX	XX		
FN	XX	DE10102338-A1.	
XX	XX		
PD	XX	25-JUL-2002.	
XX	XX		
PF	XX	19-JAN-2001; 2001DE-01002338.	
XX	XX		
PR	XX	19-JAN-2001; 2001DE-01002338.	
XX	XX		
PA	XX	(RADI) BASF PLANT SCI GMBH.	
XX	XX		
PI	XX	Lerchl J, Duwenig B, Bischoff P, Heinz E, Drexler H, Scheffler J;	
XX	XX		
DR	XX	WPT; 2002-675961/73.	
DR	XX	P-PSDB; ABG73606, ABG73607.	
XX	XX		
PT	XX	New expression cassette for plant genes, useful for preparing transgenic	
PT	XX	plants that have increased production of polyunsaturated fatty acids.	
XX	XX		
FS	XX	Example 13; Page 140-154; 188pp; German.	
XX	XX		
CC	XX	This invention describes novel expression cassette (EC) containing at	
CC	XX	least one each of plant promoter (P) and structural gene (SG) expressed	
CC	XX	in plants, flanked by specific restriction enzyme (RE) recognition sites.	
CC	XX	The EC has the structure (L1-P-SG-12) _n where L1 = is a polylinker	
CC	XX	(ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker	
CC	XX	sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing	
CC	XX	sequences and n = 1-3. The invention discloses a vector containing this	
CC	XX	EC, an organism containing the EC or the vector and a transgenic plant	
CC	XX	containing a (non-)functional nucleic acid in the vector. Transgenic	
CC	XX	plants e.g. linseed can be prepared with improved production of fatty acid	
CC	XX	esters with an increased content of polyunsaturated fatty acids (PUFA),	
CC	XX	useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.	
CC	XX	PUFA are known to reduce levels of cholesterol in the blood and to	
CC	XX	protect against heart disease. The expression cassettes of the invention	
CC	XX	provide increased and more efficient production of fine chemicals	
CC	XX	(especially PUFA), including seed-specific production. This sequence	
CC	XX	represents a nucleic acid sequence used to illustrate the method of the	
CC	XX	invention	
XX	XX		
SO	XX	Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;	

Alignment Scores:		
Pred. No.:	1.55e-155	Length: 15430
Score:	1475.00	Matches: 281
Percent Similarity:	69.88%	Conservative: 74
Best Local Similarity:	55.31%	Mismatches: 117
Query Match:	56.84%	Indels: 36
DB:	6	Gaps: 6

US-09-980-468-2 (1-483) x ABQ76796 (1-1543C)

Qy 1 MetAlaLeuValThrAspPheLeuAcs:PheLeuGlyThrThr-----TrpSerLys 17
|||:::|| ::|||::| ::::::: :::| | ||||
Db 13385 ATGTCTCTTTCAGCGACTTTCTTCAGTAATGTCTTCAACTGTTGGTTCGTGGACGGA 1344

DR WE: 2002-644810/70.
 DR 2-ESDB; ABB98278, ABB98277, ABB98274.
 XX
 PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
 PT animal or human nutrition, by transforming organism with desaturase gene
 PT from Phaseodactylum tricornutum.
 XX
 PS Example 1: Page 154-170; 182pp; German.
 XX
 CC The invention relates to preparing (M1) fatty acid esters (I) with an
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing
 CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (claimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC bioengineering method can produce (II) on a useful scale). The present
 CC sequence is that of the pUC19 based plant specific expression vector
 CC (ABV74273) expressing the Physcomitrella patens elongase (ABB98278) and
 CC the Phaseodactylum tricornutum desaturase (ABB98277 and ABB98274) of the
 CC invention. (Updated on 07-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,92e-155 Length: 17752
 Score: 1475.00 Matches: 281
 Percent Similarity: 69.88% Conservative: 74
 Best Local Similarity: 55.31% Mismatches: 117
 Query Match: 56.84% Indels: 36
 DB: 6 Gaps: 6

US-09-980-468-2 (1-493) x ABV74275 (1-17752)

Qy 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TyrSerLys 17
 Db 13385 ATGCTCTCTCAGCGACTTCTTCAGTATGTCGTTCACTGTTGCTCGAGCGTA 13444
 Qy 18 TyrSerValThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
 Db 13445 CACAGTATACAACTTTGAAG-----CGCTGACGAGTAAGAAG 13483
 Qy 38 LysValSer----- 40
 Db 13484 CGTGTTCGGAAGCGCTGCGTGCATGTATATATCAGCTGAGTTTCAGAAATTCGAGT 13543
 Qy 41 -----AlaGln:GlyLysThrAlaGlyGlnTyrLeuArgGlnArgSer 54
 Db 13544 ACCCAGGGAACCTGGAGGCACTCGCAGAAATCAGTGTGAAGCCACGAGCAAGGTCA 13603
 Qy 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
 Db 13604 TCTCAGTGGGAAGAG---TCGACACACCCCTATCAGAAGTAGCAGTACACCAAGCCA 13660
 Qy 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
 Db 13661 AGCGATTGCTGGATTGTTGTAATAAACAGGTGTATGATGTTTCATTTTCGAGCGAG 13720
 Qy 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
 Db 13721 CATCCCGAGGAGTACAGTATTAGTACTATTTCGAGCAGACGCGCAGAGATGTTTCTCT 13780
 Qy 115 ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
 Db 13781 AGTTTTTCATGCGCTCTACATGGAATAATCTTCAAGACTTTTACATTGGTGGAGTGGAG 13840
 Qy 135 ArgGluGlu:uProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal 154

Db 13941 AGGTTGGAGCCGACTCCAGAGCTGCTGAAGATATCCGAGAAATGAGAGCTCTTTTCCTG 13900
 Qy 155 ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
 Db 13901 AGGAGCAACATTTTCAAAAGTTTCGAAATTTGATATGTTATGAGCTGCTCAGCAATGTT 13960
 Qy 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
 Db 13961 GCTATTTTGTGCGAGCAATTCGCAATAATATGTTGGAGCAAGACTATTTTCAGCGGTTTG 14020
 Qy 195 LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214
 Db 14021 GCTTCAGTTGTTGATGGCTCTGTTTCCACAGTGGGATGGCTATCCCATGATTTT 14080
 Qy 215 LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
 Db 14081 CTCCACAATCAGGTGTTTGGAGACACGGCTGTTAATGAAGTTGTCGGGTATGTCGCTG 14140
 Qy 235 AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisThr 254
 Db 14141 AACGCCGTTCTGGGTTTGTAGTACAGGGTGGTGGAGGAGAACATAAAGCTTCATGCT 14200
 Qy 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
 Db 14201 GCTCCAAATGATGGATCAGACTTACCAACCAATGATGAGATATTTGATACTCTCCC 14260
 Qy 275 IleIleAlaTrpSerCysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
 Db 14261 CTCAATTCGCTGGAGCAAGGACATATCTGCCCACAGTTGAGAAATAAGACATCTTCGGAATC 14320
 Qy 295 LeuGlnTyrGlnHisTyrMetIleLeuProIleLeuPheMetAlaArgTyrSerTrpThr 314
 Db 14321 CTCCAATACCAAGCATCTGTTCTTCATGGGTCTGTATTTTTCGCCCGTGGTATGGCTC 14380
 Qy 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
 Db 14381 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCCTGTCGACAGGTGTGTGGAG 14440
 Qy 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
 Db 14441 AAGGGAACATGTTCTGTTTCACTACTTTTGTGTCGGGACAGCGTGTATCTTCTCCCT 14500
 Qy 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeu 374
 Db 14501 GGT---TCGAAGCCATTAGTATGGATGGCGTGACTGAGCTCATGTCGGGATGCTGCTG 14557
 Qy 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
 Db 14558 GCCTTGTATTTGTACTTAGCCACAAATGGGATGGAGGTTTATATTCGCTTAAGAAATTC 14617
 Qy 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
 Db 14618 GTGAGTGACAGATCGTATCCACACGGGATCAAAAGCAACATATTCACAGCTGTTTC 14677
 Qy 415 ThrGlyGlyLeuAspThrGlnIleGluHisIleLeuPheProThrMetProArgHisAsn 434
 Db 14678 ACTGGTGGCTTAAACAGGCAATAGAGCATCTCTTTTCCCAACAAATGCCAGGATATAT 14737
 Qy 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
 Db 14738 TTAACAAATAGCACCTAGAGTGGAGGTGTTCTGTAAGAAACACGGTCTGGTGTACGAA 14797
 Qy 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
 Db 14798 GACGTATCTATTGCTACCGGCACTTGCAGAGGTTTGAAGGCAATTGAAGAAATGCGCG--- 14854
 Qy 475 GluAlaSerIleArgLeuHisAla 482
 Db 14855 GAGGCTGGCGAGCAGCATGCT 14878
 RESULT 11
 ABQ76797

ID ABQ76797 standard; DNA; 17752 BP.
 XX AC ABQ76797;
 XX 25-MAR-2003 (first entry)
 XX DE pBAR1 encoding delta6 elongase, delta6 and delta5 desaturase.
 XX Promoter; expression cassette; structural gene; plant; transgenic;
 XX linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 XX animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 XX heart disease; seed-specific; ds.
 XX OS Physcomitrella patens.
 XX OS Phaeodactylum tricornutum.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT CDS 11543..12415
 XX FT /*tag= a
 XX FT /product= "delta6 elongase"
 XX FT /note= "from Physcomitrella patens"
 XX FT CDS 13313..14890
 XX FT /*tag= b
 XX FT /product= "delta6 desaturase"
 XX FT /note= "from Physcomitrella patens"
 XX FT CDS 15791..17200
 XX FT /*tag= c
 XX FT /product= "delta12 desaturase"
 XX FT /note= "from Phaeodactylum tricornutum"
 XX DE10102338-Al.
 XX
 XX PD 25-JUL-2002.
 XX
 XX PF 19-JAN-2001; 2001DE-01002338.
 XX
 XX PR 19-JAN-2001; 2001DE-01002338.
 XX
 XX PA (BADI) BASF PLANT SCI GMBH.
 XX
 XX PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
 XX WPI: 2002-675961/73
 XX P-PSDB; ABG73608, ABG73609, ABG73610.
 XX
 XX PT New expression cassette for plant genes, useful for preparing transgenic
 XX plants that have increased production of polyunsaturated fatty acids.
 XX
 XX PS Example 13; Page 158-174; 188pp; German.
 XX
 XX CC This invention describes novel expression cassette (EC) containing at
 XX least one each of plant promoter (P) and structural gene (SG) expressed
 XX in plants, flanked by specific restriction enzyme (RE) recognition sites.
 XX The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker
 XX (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
 XX sequences reproduced (ABQ76799-ABQ7800) or equivalent RE-site-containing
 XX sequences and n = 1-3. The invention discloses a vector containing this
 XX EC, an organism containing the EC or the vector and a transgenic plant
 XX containing a (non-)functional nucleic acid in the vector. Transgenic
 XX plants e.g. linseed can be prepared with improved production of fatty acid
 XX esters with an increased content of polyunsaturated fatty acids (PUFA),
 XX useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
 XX PUFA are known to reduce levels of cholesterol in the blood and to
 XX protect against heart disease. The expression cassettes of the invention
 XX provide increased and more efficient production of fine chemicals
 XX (especially PUFA), including seed-specific production. This sequence
 XX represents a nucleic acid sequence used to illustrate the method of the
 XX invention
 XX
 XX SQ Sequence 17752 B2; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;
 Alignment Scores:

Pred. No.:	1.92e-155	Length:	17752
Score:	1475.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	6	Gaps:	6

US-09-980-468-2 (1-483) x ABQ76797 (1-17752)

Qy	1	MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----	TriSerLys	17
Db	13385	ATGTCCTCTTCACGGACTTCTTCAGTATGTCGTCCTCACTGTTGGTTCGTGGAGCGTA		13444
Qy	18	TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys		37
Db	13445	CACAGTATACAACTTTGAAG-----CGCTTCACGAGTAAGAAG		13483
Qy	38	LysValSer-----		40
Db	13484	CGTGTTCGGAAAGCGCTCGCTGCAATGATATATCAGCTGAAGTTCAGAAATTCGAGT		13543
Qy	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer		54
Db	13544	ACCCAGGGAACCTGGCGAGGCACTCCAGAAATCAGTCGTGAAGCCACGAGACGAAGTCA		13603
Qy	55	ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro		74
Db	13604	TCTCAGTGGGAAGAAG---TCGACACACCCCTATCAGAAGTAGCAGTACACACACGCCA		13660
Qy	75	GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp		94
Db	13661	AGCGATTGCTGGATTGTTGTAAAAACAAGGTGATGATGTTTCAATTTGGGACGAG		13720
Qy	95	HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla		114
Db	13721	CATCCGGAGGATCAGTTTATAGTACTTATTTGGACGAGACGGCACAGATGTTTCTCT		13780
Qy	115	ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla		134
Db	13781	AGTTTTTCATCGAGCTTTCATCGAAAAATTTCTTCAAGCATTTTACATTGGTGAGTGAG		13840
Qy	135	ArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal		154
Db	13841	AGGTTGGAGCGGACTCCAGAGCTGCTGMAAGATTTCCGAGAAATGAGAGCTCTTTCTCG		13900
Qy	155	ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla		174
Db	13901	AGGAGGCAACTTTTCAAAAGTTCGAAATTTGATCTATGTTATGAAGCTGCTCAGCAATGT		13960
Qy	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal		194
Db	13961	GCTATTTTCTCGGAGCATTTGCAATATATGTTGGAGCAGAGCATTTTTCAGCGGTTTG		14020
Qy	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe		214
Db	14021	GCITTCACCTTGATGATGGCTCTGTTGTTCCACAGTGGGATGGCTATCCCATGATTTT		14080
Qy	215	LeuHisGlnIleValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly		234
Db	14081	CTCCACATCAGGTGTTTGAGACACGCTGGCTTAAATCAAGTTGTCGGGTATGTATCGGC		14140
Qy	235	AsnCysValLeuGlyPheSerValSerTyrTrpArgThrLysHisAsnIleHisHisThr		254
Db	14141	AACGCCGTTCTGGGGTTTATGACAGGTGGTGGNAGAGAGCATATACCTTCATCATGCT		14200
Qy	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro		274
Db	14201	GCTCCAAATGAATGCGATCAGACTTACCAACCAATGATGAAGATATTGATCTCTCCC		14260
Qy	275	IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal		294
Db	14261	CTCATTCCTGGAGCAAGGACATCTGCGCCACAGTTCGAGAAATTAAGACATTTCTTCGGAATC		14320

QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpTrp 314
 Db 14321 CTCGAATACCAAGCACTGCTCTCTATGAGTGGTCTGTTATTTTCGCCCGTGGTATGGCTC 14380
 QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
 Db 14381 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGGCTCTACCTGTGCACAGGTGTGTGGAG 14440
 QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
 Db 14441 AAGGGAAGTGTCTCTCTTCACTACTCTTTGGTTCGTGGCAGACGGTGTCTATCTTCCCT 14500
 QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeu 374
 Db 14501 GGT---TGGAGGCCATTAGTATGGATGGCGGTGACTGAGCTCATCGCGCATGCTGCTG 14557
 QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
 Db 14558 GGCITTTGTTTGTACTTAGCCACATGGGATGGAGTGTATATTCGTCTAAGAAATTC 14617
 QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
 Db 14618 GTGAGTCACAGATCGTATCCACAGCGGATATCAAGGAAACATATTCACGACTGCTTC 14677
 QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
 Db 14678 ACTGTGGCTTTAACAGGCAATAGAGCATCATCTTTTCCCAACATGCCCCAGGCATAT 14737
 QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
 Db 14738 TTAACAAATAGACCTAGAGTGGAGGTGTTCTGTAGAAACACGGTCTGTGTACGAA 14797
 QY 455 AsnValSerValGlyValAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
 Db 14798 GACGTATCTATTGTACCGCACTTGCAGAGGTTTTCAGAAAGCATTCAGAGGAAGTCGCG--- 14854
 QY 475 GluAlaSerIleArgLeuHisAla 482
 Db 14855 GAGGCTGGCGAGCAGCAGCATGCT 14878

RESULT 12

AAF25731
 ID AAF25731 standard; DNA; 520 BP.
 AC AAF25731;
 DT 06-APR-2001 (first entry)
 DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 5.
 DE Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic; ds.
 XX Ceratodon purpureus.
 XX WO200075341-AL.
 PN 14-DEC-2000.
 PD 07-JUN-2000; 2000WO-EP005274.
 PF 07-JUN-1999; 93DE-01025718.
 PR 22-DEC-1999; 93DE-01062409.
 XX (BADI) BASF AG.
 XX Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
 XX WPI; 2001-112150/12.
 DR P-PSDB; AAB46437.
 XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for

PT producing plant oils with increased content of unsaturated fatty acids.
 XX Example 6; Page 51; 69pp; German.
 XX This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (IIa); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants for other organisms that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids

XX Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,978-95 Length: 520
 Score: 925.00 Matches: 172
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.42% Mismatches: 0
 Query Match: 35.65% Indels: 0
 DB: 4 Gaps: 0

US-09-980-468-2 (1-483) x AAF25731 (1-520)

QY 251 IleHisHisThrAlaProAsnGluCysAspGluInTyrThrProLeuAspGluAspIle 270
 Db 2 ATTCATCATCTAGTCTCCGATAGTGGAGCAACAGTACACCTCTACAGAGACATT 61
 QY 271 AspThrLeuProIleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArg 290
 Db 62 GATACTCTCCCATCATTCCTGGAGCAAGGAAATTTGGCCACCTTGAGAGCAAGAGA 121
 QY 291 IleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArg 310
 Db 122 ATTTTGGAGTGTCTCGATATCAGCACTACATGATTCTGCTCTATTGTTTCATGGCCCGG 181
 QY 311 TyrSerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLys 330
 Db 182 TACAGTTGGACTTTTGGAGTTTGTCTTTCACATTCAATCTCTGATTGGACGACCAAG 241
 QY 331 GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPhe 350
 Db 242 GCAATTGATAGAGAGCAAGTGTGCTTTTCACTACGCTGTGTTCAGTTGGGTGCTGCTC 301
 QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370
 Db 302 CATATTTTGGCGGTGTCTGCTAAGCTCTCTGCTGGATGGTAGGCACTCAGCTTGTGGCC 361
 QY 371 GlyLeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu 390
 Db 362 GGTITTTGTTTGGGATCTGTTTACGTTGAGTACATTCAGAAAGAGAGGTTTACATGAA 421
 QY 391 SerLysAspPheValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPhe 410
 Db 422 TCGAAGGACTTCGTGAGAGCCAGGTATTATACACCCGTAACACCAAGGAGGCTGCTTC 481
 QY 411 AsnAspTrpPheThrGlyLeuAspThrGlnIleGlu 423
 Db 482 AACGATTGTTTCACTGGGGGACTCGACACCCAGATTGAG 520
 RESULT 13
 AAZ47129

Db 1261 AAAAGTACATGTCCTGATACACACACCACCGGTATGATCGAGGAACTGCAGAGGCTTTT 1320

QY 467 LysAlaLeuLysGluLeuAlaAspGluAlaSer 477

Db 1321 AGCCGTC-GAAGGAGGTCTCCAAAGGCTGCTCC 1353

RESULT 14

AAF25234

ID AAF25234 standard; DNA; 1374 BP.

XX AAF25234;

XX 30-APR-2001 (first entry)

DE Nucleotide sequence of a fungal delta6 desaturase.

KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;

KW eicosanoid; nutrition; infant formula; dietary supplement;

KW dietary substitute; animal feed; ss.

XX Mortierella alpina.

FH Key Location/Qualifiers

FT CDS 1..1374

FT /*tag= a

FT /product= "delta6 desaturase"

XX WO200104636-A1.

PN 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US019011.

XX 12-JUL-1999; 99US-00351525.

XX (UYOH-) UNIV OHIO.

PA Kopchick JJ, Kelder B;

XX WPI; 2001-132622/18.

DR P-PSDB; AAB31684.

XX New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or animal feed formulations.

PS Disclosure; Fig 8; 93pp; English.

CC The present sequence encodes a delta6 desaturase. The desaturase polynucleotide sequence was used to transfect mammalian cells, to produce animal cells expressing a desaturase gene and/or an elongase gene.

CC Compositions comprising cells of the invention are useful for synthesizing essential fatty acids, their derivatives or downstream

CC products, as well as altered levels of long-chain polyunsaturated fatty acids and eicosanoids. The compositions are useful in nutritional

CC formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be

CC used as fat free media or as research reagents

XX SQ Sequence 1374 BP; 257 A; 386 C; 378 G; 353 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,01e-85	Length:	1374
Score:	841.50	Matches:	177
Percent Similarity:	55.21%	Conservative:	72
Best Local Similarity:	39.25%	Mismatches:	159
Query Match:	32.43%	Indels:	43
DB:	5	Gaps:	10

US-09-980-468-2 (1-483) x AAF25234 (1-1374)

QY	62	ThrTyrSerLeuAlaAspVal	-----AlaSerHisAspArg	73
Db	25	ACGTTTACTCGGCCCGAGGTTTGAATGCGAGGCTCTGAATGAGGCAAGAGATGCC		84
QY	74	ProGlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp		93
Db	85	GAGGCACCTTCTTGTGATGATCATCGACACAAAGGTGTACGATGTCGCGAGTTCTGCTCCT		144
QY	94	AspHisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPhe		113
Db	145	GATCATCCCGGTGGAAGTGTGATTTCTCAGCACGTTTGGCAAGGACGCGACTGACGCTTT		204
QY	114	AlaThrPheHisProProAlaAlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeu		133
Db	205	GACACTTTTACCCCGAGGCTGCTTGGAGACTCTTCCCACTTTTACGTGTGGTATTT		264
QY	134	-----AlaArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArg		150
Db	265	GACGAGCGACGCGCGATATCAAGATGATGACTTTGCGCGCGAGGTCCGCAAGCTCGT		324
QY	151	AlaGluPheValArgGluGlyLeuPheLysSerSerLysAlaTyrPheLeuLeuGlnThr		170
Db	325	ACCTTGTTCAGTCTCTTGGTTACTACGATTCCTCAAGGCATACTACGCTTTCAAGTC		384
QY	171	LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr	-----AspLys	188
Db	385	TGCTTCAACCTTCGATCTGGGGTGTTCGACGCTGATTTGGCCCAAGTGGGCGCAGACC		444
QY	189	SerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGly		208
Db	445	TCGACCTTCGCCAACGCTCTCGGCTGCGCTTTTGGTCTGTTTGGCAGCAGTGGCGGA		504
QY	209	TrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhe		228
Db	505	TGGTTGGCTCAGCACTTTTGCATCACAGCTCTTCCAGGACCGTTTCTCGGCTGATCTT		564
QY	229	PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpTyrPheThrLys		248
Db	565	TTGCGGCTTCTTGGAGGTGTCGCGAGGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCT		624
QY	249	HisAsnIleHisThrAlaProAsnGluCysAspGlnGlnTyrThrProLeuAspGlu		268
Db	625	CACCACTCACCCACCGCGCGCCCAAGTCCACGGCGAG-----GATCCC		669
QY	269	AspIleAspThrLeuProIleLeuAlaTrpSerLys-----GluIleLeuAlaThr		285
Db	670	GACATTGACACCCACCTCTGTGACCTGGAGTGACATGCGTTGGAGATGTTCTCGGAT		729
QY	286	ValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeu	-----	303
Db	730	GTCCCAGATGAGGAGTGTACCCGATG-----TGGTCGGTTTCATGGTCTGACCCAG		783
QY	304	-----ProLeuLeuPheMetAlaArgTyrSerTrpThrPheGlySerLeu		318
Db	784	ACCTGGTTTACTTCCCATCTCTCGTTGCGCGTCTCTCTGCTGCTGCCATTCATT		843
QY	319	LeuPheThrPheAsnProAspLeuSerThrLys-----		330
Db	844	CTCTTTGTGCTG---CCTAACGTCAGGCCCAACAGCCCTCGCGCGCGGTGTCGCCATC		900
QY	331	GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPhe		350
Db	901	TGTTGGTCGACGAGCTGCTGCTGGATGATGACCTGGACCTGTACCTGCCACCATGTC		960
QY	351	HisIleLeuGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla		370
Db	961	CTGTTTCATCAAGATCCCGTCAACATGCTGGTGTACTTTTGGTGTGCGCGCGGTGTC		1020
QY	371	GlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu		390
Db	1021	GGAAACTTGTGGCGATGCTGTTCTCGCTCAACCAACAGGATGCTGCTGATCTCGAAG		1080
QY	391	SerLys-----AspPheValArgAlaGlnValIleThrThrArgAsnThrLys		406

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DB 1081 GAGGAGGGCGTGCATATGATTCTTCACGAGCAGATCATCATCGGGTGGTGATGCCAC 1140
QY 407 ArgGlyTyrPheAsnAspTyrPheThrGlyGlyLeuAspThrGlnIleGluHisLeu 426
DB 1141 CCGGGTCTATTGGCCACTGGTTCACGGGTGGATTGAACTATCAGATCGAGCACCATTG 1200
QY 427 PheProThrMetProArgHisAspTyrProLysIleAlaProGlnValGluAlaLeuCys 446
DB 1201 TTCCTTCGATGCTCGCCACACTTTTCAAGATCCAGCTCTCTCGAGACCTGTGC 1260
QY 447 LysLysHisGlyLeuGlyTyrAspAsnValSerValValGlyAlaSerValAlaValVal 466
DB 1261 AAAAAGTCAATGTCGATACACACACCCGATGATCGAGGAACCTCGAGAGGTCTTT 1320
QY 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477
DB 1321 AGCGTCTGACGAGGTCTCCAGGCTGCTCC 1353
RESULT 15
AAV63624
ID AAV63624 standard; cDNA; 1617 BP.
XX
AC AAV63624;
XX
DT 15-FEB-1999 (first entry)
DE cDNA encoding a delta-6 desaturase enzyme.
XX
KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition;
KW inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes;
KW eczema; platelet aggregation; vasodilation; cholesterol level;
KW endometriosis; premenstrual syndrome; myalgic encephalomyelitis;
KW chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome;
KW hypertension; inflammatory skin disorder; ss.
XX
OS Mortierella alpina.
XX
FH Key
FT 71..1444
FT CDS
FT /*tag= a
FT /product= "delta-6 desaturase"
XX
PN WO9846763-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007126.
XX
PR 11-APR-1997; 97US-00834655.
XX
PA (CALJ ) CALGENE LLC.
PA (ABBO ) ABBOTT LAB.
XX
PI Knutzen D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
PI Leonard AE;
XX
DR NPI; 1998-594582/50.
DR P-PSDB; AAW84137.
XX
PT New isolated fatty acid desaturase enzymes - used for the production of
PT polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions,
PT nutritional compositions, cosmetics or animal feed.
XX
PS Claim 1; Fig 3A-E; 165pp; English.
XX
CC The present sequence encodes a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of the
CC invention. The specification describes methods for desaturating a fatty
CC acid and for producing a desaturated fatty acid by expressing increased
CC levels of a desaturase. The present desaturase is an enzyme which
CC introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty
CC acid molecule. The enzyme can be used for desaturating fatty acids. The

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CC enzyme can be used to produce polyunsaturated fatty acids, which can be
CC used for treating malnutrition, in pharmaceutical compositions, in
CC cosmetics or in animal feed. The polyunsaturated fatty acids can be used
CC for treating e.g. restenosis after angioplasty, inflammation, rheumatoid
CC arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood
CC pressure. They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent gastro-
CC intestinal bleeding and other side effects caused by non-steroidal anti-
CC inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral
CC infections, treat AIDS, multiple sclerosis, acute respiratory syndrome,
CC hypertension and inflammatory skin disorders
XX
SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

```

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Alignment Scores:
Pred. No.: 5,13e-85 Length: 1617
Score: 841.50 Matches: 177
Percent Similarity: 55.21% Conservative: 72
Best Local Similarity: 39.25% Mismatches: 159
Query Match: 32.43% Indels: 43
DB: 2 Gaps: 10

```

US-09-980-468-2 (1-483) x AAV63624 (1-1617)

```

QY 62 ThrTyrSerLeuAlaAspVal-----AlaSerHisAspArg 73
DB 95 ACCTTTACTCGGCCGAGGTTTGAATGCGAGGCTCTGAATGCGGCACAGAGGATGCC 154
QY 74 ProGlyAspCysTyrMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp 93
DB 155 GAGGCACCCTCTTGATGATCATCGACACAGGTGTACGATGTCCGCGAGTTGCTCCCT 214
QY 94 AspHisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPhe 113
DB 215 GATCATCCCGGTGGAAGTGTGATTCTCACGACAGTTTGGCAAGACGCGCATCGCTTT 274
QY 114 AlaThrPheHisProProAlaAlaTyrLysGluLeuAsnAspTyrTyrIleGlyAspLeu 133
DB 275 GACACTTTTCCACCCGAGGCTGCTTGGGAGACTCTTCCCAACTTTTACAGTTGTGATATT 334
QY 134 -----AlaArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArg 150
DB 335 GACGAGAGCGACCGCGATATCAAGATGATGACTTTCGCGCGAGGTCCGCAAGCTGCGT 394
QY 151 AlaGluPheValargGluGlyLeuPheLysSerSerLysAlaTyrPheLeuLeuGlnThr 170
DB 395 ACCTTGTTCAGTCTCTTGGTTACTAGGATTTCCCAAGGCATACACGCTTCRAGGTC 454
QY 171 LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr-----AspLys 188
DB 455 TCGTTCAACTCTGCATCTGGGGTTTGTCCACGGTCATTGTGGCAAGTGGGGCCAGACC 514
QY 189 SerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGly 208
DB 515 TCGACCCCTCGCCAAAGTGTCTCGGTGCGCTTTGGGTCTGTCTGCGCAGTGGCGA 574
QY 209 TrpLeuAlaHisAspPheLeuHisGlnValPheGluAsnArgThrAlaAsnSerPhe 228
DB 575 TGGTGTGCTCAGCACTTTTTCATCACAGGTCTTCCAGGACCGTTTCTGGGGTGAATCTT 634
QY 229 PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpTyrArgThrLys 248
DB 635 TTGGCGCCCTTCTGGAGAGGTCTGCCAGGGCTTCTCGTCTCTGTGGTGAAGGACAAG 694
QY 249 HisAsnIleHisThrAlaProAspGluCysAspGluGlnTyrThrProLeuAspGlu 268
DB 695 CACAACACTCACCGCGCGCCCAACAGTCCACGGCGAG-----GATCCC 739
QY 269 AspIleAspThrLeuProIleIleAlaTrpSerLys-----GluIleLeuAlaThr 285
DB 740 GACATTTGACACCCACCTCTGTTGACCTGGAGTGAATGCGTTGGAGATGTTCTTGAT 799

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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:00:51 ; Search time 18 Seconds

(without alignments)

1397.216 Million cell updates/sec

Title: US-09-980-468-2

Perfect score: 2595

Sequence: 1 MALVTDFINFLGTWSKYSV.....AVVKALKEIADEASIRLHAH 483

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 3.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	500.5	19.3	444	1 PADS_BRAPE	Q9d871 brachydario
2	200	7.7	359	1 LACD_SYNY3	Q98871 synechocyst
3	193.5	7.5	132	1 CYB5_BORGF	O04354 borago offi
4	190.5	7.3	137	1 CYB5_ORYSA	P49100 oryza sativ
5	179.5	6.9	136	1 CYB5_TOBAC	P49098 nicotiana t
6	172.5	6.6	135	1 CYB5_CUSRE	P49097 cuscuta ref
7	172	6.6	135	1 CYB5_TOBAC	P49099 nicotiana t
8	170.5	6.6	134	1 CY52_ARATH	O48845 arabidopsis
9	166.5	6.4	900	1 NIA_LOTJA	P39869 lotus japon
10	164	6.3	918	1 NIA_CUCMA	P17569 cucurbita m
11	162.5	6.3	435	1 FD3D_ARATH	P48622 arabidopsis
12	160.5	6.2	864	1 NIA_VOLCA	P36841 volvox cart
13	160	6.2	120	1 CYB5_YEAST	P40312 saccharomyc
14	160	6.2	890	1 NIA2_PHAVU	P39866 phaseolus v
15	159.5	6.1	380	1 FD3E_PHAU	P42291 phaseolus a
16	158.5	6.1	460	1 FD3C_RICCO	P48619 ricinus com
17	157	6.1	124	1 CY51_SCHPO	O94391 schizosacch
18	157	6.1	890	1 NIA2_SOYBN	P39870 glycine max
19	154.5	6.0	318	1 NIA_CHLVU	Q01170 chlorella v
20	154	5.9	414	1 CYBR_DROME	P19967 drosophila
21	154	5.9	591	1 CYB2_YEAS-	P00175 saccharomyc
22	154	5.9	886	1 NIA1_SOYBN	P54233 glycine max
23	153.5	5.9	134	1 CY51_ARATH	Q42342 arabidopsis
24	153	5.9	917	1 NIA1_ARATH	P11832 arabidopsis
25	153	5.9	917	1 NIA2_ARATH	P40934 arabidopsis
26	150	5.8	134	1 CYB5_BRACL	P11035 brassica ol
27	150	5.8	911	1 NIA1_BRANA	P39867 brassica na
28	149	5.7	881	1 NIA1_PHAVJ	P39865 phaseolus v
29	149	5.7	904	1 NIA2_TOBAC	P08509 nicotiana t
30	149	5.7	911	1 N-A2_BRANA	P39868 brassica na
31	148.5	5.7	146	1 CYM5_RAT	P04166 rattus norv
32	148.5	5.7	453	1 FD3C_SOYBN	P48621 glycine max
33	148	5.7	384	1 SC57_YEAST	Q03529 saccharomyc

34 147.5 5.7 902 1 NIA_PHYIN
35 147 5.7 131 1 CYB5_RHIST
36 146.5 5.6 380 1 FD3E_SOYBN
37 146.5 5.6 386 1 FD3E_ARATH
38 143.5 5.5 926 1 NIA_SP-OL
39 143 5.5 443 1 FD6C_BRANA
40 142 5.5 129 1 CY52_SCHPO
41 142 5.5 911 1 NIA_LYCES
42 141.5 5.5 379 1 FD3E_TOBAC
43 141 5.4 383 1 FD62_SOYBN
44 141 5.4 898 1 NIA_BETVE
45 141 5.4 909 1 NIA_PETHY

P39864 phytophthor
Q9hiv1 rhizopus st
P48625 glycine max
P48623 arabidopsis
P23312 spinacia ol
P48627 brassica na
Q9usm6 schizosacch
P17570 lycopersico
P48626 nicotiana t
P48631 glycine max
P27783 betula verr
P36859 petunia hyb

ALIGNMENTS

RESULT 1
FADS_BRARE
ID FADS_BRARE STANDARD; PRT; 444 AA.
AC Q9DEX7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).
GN FADS2 OR FADS26.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21592990; PubMed=11724940;
RA Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,
Sargent J.R., Teale A.J.;
RT "A vertebrate fatty acid desaturase with delta5 and delta6
activities.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).
CC -!- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6
activities. May represent a component of the polyunsaturated fatty
acid biosynthesis pathway.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
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CC -----
CC EMBL; AF309556; AAC25710.1; --
CC HSSP; P00173; 1JEX.
CC ZFIN; ZDB-GENE-0111212-1; fads2.
CC InterPro; IPR001199; Cyt B5.
CC InterPro; IPR005804; FA_Desat_fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC ProDom; PD000612; Cyt B5; 1.
CC ProDom; PD001091; FA_Desat_fam; 2.
CC PROSITE; PS00191; CYTOCHROME_B5_1; FALSE_NEG.
CC PROSITE; PS02055; CYTOCHROME_B5_2; 1.
CC Fatty acid biosynthesis; Oxidoreductase; Heme.
KW DOMAIN 18 95 HEME-BINDING.
FT METAL 53 53 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 76 76 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 444 AA; 52032 MW; 6AA25A1DC0F65 CRC64;

Query Match 19.3%; Score 500.5; DB 1; Length 444;
 Best Local Similarity 28.8%; Pred. No. 1.5e-34;
 Matches 130; Conservative 78; Mismatches 164; Indels 79; Gaps 16;

QY 62 TYSADVASHDRPGDWMIVKEKVDISFPADHPCG-TWISTYFGDGDVDFATFHP-- 118
 DB 20 SYTVEVQKHGQDQWVVERKVNVSQWKKHPCGLRILGHYAGEDATEATFHPML 79

QY 119 PAWKGNDYITGLAREFLDE-----LLKDYDRMRAEFVREGLFKSKAWFLLOTLI 172
 DB 80 QLVKRYKELLIGELASPSQDRQKNAALVEDFRALREERLEBAEGCFKQPLFFALHGH 139

QY 173 KRALFAS-ATICDYKSYNA-IVLSASLMGLFVQCCGWLADHLEHESQVFNRTANSFFGY 232
 DB 140 ILLLEAIAFMVWYFTGWTINTLIVAVILATAQSQAGWLQHDFFGH-SVFKTSGMNLVHK 199

QY 232 LFGNCVLFSGSVNRKTHHTAPNECDQVTPLEDIDITLPIAWSKKELIATVE-- 287
 DB 200 FVIGHLKASAGWNHHRHQHAKNIFXK-----DFDVMML-----NAPVGNVQVPEY 249

QY 288 SKRILRVLOYQHYMILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHYAWPSW 347
 DB 250 GVKKIKHLPNH-----QHKY-----PFFIGPPL-----LIP-----VVFQF 281

QY 348 AAFH--ILFGVAKPLAMWA-----TELV-----AGLLGF-----VFTLS 381
 DB 282 QIFHNHISGMWMDLLWCISYVRYFLCYTFQGVFWAILFNVPFMESHWFVWVTQMS 341

QY 382 HNGKEV-YNESKDFVRAQVTTTNRKGFNDWFTGGLDQIBHHLFPPTVPRNYPKIAF 440
 DB 342 H.FPMNDYKQDLNSQLVATCNIEQSAENDFSGHLNFQIBHHLFPPTVPRNYPKIAF 401

QY 441 QVEALCKHGLEVDYDVSVVGASVAVKALKE 471
 DB 402 RVRAALCEKGVKQKTXGAPADILRSLEK 432

RESULT 2
 LCED_SINY3 STANDARD; PRT; 359 AA.
 AC Q08871;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
 GN DES6 OR SL0262.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP MEDLINE=93283633; PubMed=8389613;
 RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
 RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
 RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
 RT Anabaena sp. strain PCC 7120.";
 RL Plant Mol. Biol. 22:293-300(1993).
 RN [2]
 RP MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shampo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -1- CATALYTIC ACTIVITY: Linoleoyl-CoA + AH(2) + O(2) = gamma-
 CC linolenoyl-CoA + A + 2 H(2)O.
 CC -1- COFACTOR: Iron.

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DR EMBL; L11421; AAA27286.1; -;
 DR EMBL; D90914; BAA18502.1; -;
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Iron; Complete proteome.
 SQ SEQUENCE 359 AA; 41425 MW; 33FBL6SAEB98C05F CRC64;

Query Match 7.7%; Score 200; DB 1; Length 359;
 Best Local Similarity 24.0%; Pred. No. 2.6e-09;
 Matches 86; Conservative 50; Mismatches 141; Indels 82; Gaps 17;

QY 151 AETVRGLPKSSXAMFLLOTLINAA-LFAASIAATICYDKSYWALVLSA-----SLMGLF 203
 DB 25 AYFAEGLTQRDNPSMYLTKLITLWLFSA-----WAPVLFAPVIFPVLGCM 73

QY 204 VQCGWLA-----HDFLHQQVFNRTANSFFGVLFGNCVLFSGSVNRKTHN-IHHTAP 256
 DB 74 VLAIALAASFVGHGDAHNAYSNHNHINRVLTGYD--FVGLSSFLWRYRHNVLHHTT 311

QY 257 NECDEQVTPLEDIDITLPIAWSKKELIATVEKRLRVLOYQHYMILPLLFMARYSWTFG 316
 DB 132 N-----ILGHQVE-----IHGDGAVRMSPEQEHV-GIYRFQOFYIMGLYLFIPFYW-- 176

QY 317 SLLETFNPDLSTTKG-----LIEKGTVAHYAWFSNA-AHILPGVAKP--LA 361
 DB 177 ---FLYDVLVLMKGYHDKHIPPQFPLEASLIGLKLMLGVLGFLPLALGFSIPEVLI 233

QY 362 MVVATELVAGLLGFLVFTLSHNGKEVYNESKDFVR-----AQVITTRN--T 405
 DB 234 GASVTYNTYGVICTIFMLAH-----VLESTELTPDGESGAIIDDEWAIQIRTTANFAT 288

QY 406 KRGWFNDWFTGGDQTQIEHHLFTPMFRNTPKTAQVEALCKHGLEVDYDVSVVGASVA 464
 DB 289 NNDFPN-WFCGGLNHQVTHLFPNICHIPQLENIIKDVCFEGVEYKYPYTFKAAIA 346

RESULT 3
 CYB5_BOROF STANDARD; PRT; 132 AA.
 AC O04354;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Borago officinalis (Borraghe) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Boraginaceae; Borago.
 OX NCBI_TaxID=13363;
 RN [1]
 RP MEDLINE=97268723; PubMed=9108131;
 RA Savanova O., Smith M.A., Lapinskas P.A., Stohart K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borago desaturase cDNA containing an N-terminal
 RT cytochrome b5 domain results in the accumulation of high levels of
 RT delta-desaturated fatty acids in transgenic tobacco.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrion. Bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -1- SIMILARITY: Belongs to the cytochrome b5 family.

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CC -----
 CC EMBL: J79011; AAC49701.1; -
 CC HSSP: P00171; 1CVO.
 CC InterPro: IPR001199; Cyt B5.
 CC Pfam: PF00173; heme.1; 1.
 CC ProDom: PD000612; CYTOCHROME B5 1; 1.
 CC PROSITE: PS00191; CYTOCHROME B5 2; 1.
 CC PROSITE: PS0255; CYTOCHROME B5 2; 1.
 CC KW Electron transport; Transmembrane; Heme; Iron; Microsome.
 CC FT TRANSMEM 104 124 POTENTIAL.
 CC FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;

Query Match 7.5%; Score 193.5; DB 1; Length 132;
 Best Local Similarity 33.8%; Pred No. 2.6e-09;
 Matches 48; Conservative 24; Mismatches 39; Indels 31; Gaps 6;

QY 63 YSLADVASHDRPGDCMWIKVKYDISRFADHPG3-TVISTYFGDGTDFVATF-HPPA 120

DB 5 FTLEAVAHNNKSCWLLNGKVVYDTRFLEDPHGGDDVLLSAGTKDATDDPEDIGHSS 64

QY 121 AWKQNDYIGDL-----AREPDELKDYR-DMAEFVRGELFKSSKANFL 167

DB 65 AKAMLDYVYGVGDSSSPSQVYTPPKQPL-----YNPKTRBFVTK-----L 108

QY 168 LQTLNLAALFAASIATICYDKS 189

DB 109 LQFLVILGATGIRYTKS 130

RESULT 4

CYB5 ORYZA STANDARD; PRT; 137 AA.

AC P43100;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriophytidae; Cryzeae; Oryza.
 ON NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Callus.
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting."
 RL plant Mol. Biol. 25:527-537(1994).

CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial membrane. Bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
 CC -----
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DR EMBL: X75670; CAAS3366.1; -
 DR PIR: S46307; S46307.
 DR HSSP: P00171; 1EHB.
 DR Gramene; P49100; -
 DR InterPro: IPR001199; Cyt B5.
 DR Pfam: PF00173; heme.1; 1.
 DR PRINTS: PR00363; CYTOCHROME B5.
 DR ProDom: PD000612; CYT B5; 1.
 DR PROSITE: PS00191; CYTOCHROME B5 1; 1.
 DR PROSITE: PS0255; CYTOCHROME B5 2; 1.
 CC KW Electron transport; Transmembrane; Heme; Iron; Microsome.
 CC FT TRANSMEM 108 128 POTENTIAL.
 CC FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 137 AA; 15296 MW; 4260C9D633E60FDA CRC64;

Query Match 7.3%; Score 190.5; DB 1; Length 137;
 Best Local Similarity 33.1%; Pred. No. 4.9e-09;
 Matches 48; Conservative 28; Mismatches 48; Indels 21; Gaps 6;

QY 54 SYQDKKPGTYSLADVASHDRPGDCMWIKVKYDISRFADHPG3-TVISTYFGDGTDFV 112

DB 2 SNDNKK--VYTLVEAVAHNNKSCWLLIGGVYNNVSKFLEDPHGGDDVLLSAGTKDATDD 59

QY 113 FATF-HPPAWQQLNDYIGDL-----AREPDELKDYR-DMAEFVRGELFKSSKA 164

DB 60 FEDVGHITTAAMDEYVYGVGDITSTIPARTKYVPPKQPHYNQKTPFIK----- 111

QY 165 WFLQTLNLAALFAASIATICYDKS 189

DB 112 --ILQFLVPLAILGLAVAIRYTKS 134

RESULT 5

CYB5 TOBAC

ID CYB5 TOBAC STANDARD; PRT; 136 AA.

AC P49088;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf.
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting."
 RL plant Mol. Biol. 25:527-537(1994).

CC -!- FUNCTION: Cytochrome b5 is a membrane bound hemoprotein which
 CC oxygenases. May play a key role in the modification by
 CC desaturation of fatty acids in the endoplasmic reticulum, which in
 CC the developing seed is utilized for membrane synthesis and in the
 CC developmentally regulated production of large amounts of storage
 CC lipids. Is involved in the reduction of cytochrome P-450 and
 CC may therefore be involved in flavonoid biosynthesis in the petals.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial membrane. Bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -!- TISSUE SPECIFICITY: Is highly expressed in developing seeds,
 CC moderately expressed in flowers, and is expressed at low
 CC levels in the leaf.
 CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
 CC -----

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DR PIR; S432CC; S49200.
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00131; CYTOCHROME_B5_2; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR E-electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127
FT METAL 40 40
FT METAL 64 64
FT METAL 64 64
SQ SEQUENCE 135 AA; 14869 MW; A36CA081A72ECBC CRC64;
Query Match 6.6%; Score 172; DB 1; Length 135;
Best Local Similarity 41.1%; Pred. No. 1.8e-07;
Matches 30; Conservative 21; Mismatches 20; Indels 2; Gaps 2;
QY 63 YSLADVASHDRPCDGMWIKVKEKVDYISRFADHPG-GTIVSTVFGDGDVDFATF-HPPA 120
DB 8 FTLAEVSNHNAKDCWLLISGKYNVTKLEDPGCGEVLSTGKDADDFEDVGHSS 67
QY 121 AKQLNDYIGDL 133
DB 68 ARAMLDYVVDI 80
RESULT 8
CY52_ARATH STANDARD; PRT; 134 AA.
ID CY52_ARATH
AC O48845;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cytochrome b5 isoform 2.
OS Arabidopsis thaliana (Mouse-ear cress).
GN Arabidopsis thaliana
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
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CC EMBL; AC003974; AAC04491.1; -.
CC PIR; T00796; T00796.
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DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR001834; Cyt B5 reductase.
DR InterPro: IPR008335; Euk Mb oxred.
DR InterPro: IPR008333; FAD binding 6.
DR InterPro: IPR001709; FPN_cyt_reductase.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR005066; Mo-co dimer.
DR InterPro: IPR000572; Oxidored molyb.
DR InterPro: IPR001433; Oxred FAD/NAD(P).
DR Pfam: PF00970; FAD binding_6; 1.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co dimer; 1.
DR Pfam: PF00175; NAD binding_1; 1.
DR Pfam: PF00174; oxidored_molyb; 1.
DR PRINTS: PR00406; CYTB5RDTASE.
DR PRINTS: PR00363; CYTOCHROME5.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; FPNCR.
DR ProDom: PD000612; Cyt B5; 1.
DR PROSITE: PS00191; CYTOCHROME B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase: Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation
FT METAL 172 172 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 226 226 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 411 411 INTERCHAIN (POTENTIAL).
FT METAL 556 556 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 579 579 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 900 AA; 101420 MW; 547C25388DD13535 CRC64;

Query Match 6.4%; Score 166.5; DB 1; Length 900;
Best Local Similarity 30.3%; Pred. No. 5.6e-06;
Matches 46; Conservative 20; Mismatches 63; Indels 23; Gaps 5;

QY 3 LVTDLFLNGLTTSKYSVYTH---SVAGNYGPTLKAKKVSAC--GKTAGQTLRQSRVOD 57
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 LWNVMGMNNCW--FRVKTNMCKPKHGEIGVFEHPTQPGNQSGGMMDRERHLEISTES 526
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 KKP-----GTYSADYASHDRPGDCWMIKVKYDYSRFRADHPGGT-VI 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 504 SRPLKKSYSPPMNTFTKXSLSEVKKNSPDSAMIIVGHVYDCTFLKDHPPGGDSI 563
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 STYFGDGTDFVATFHPPAWKQNDYYIGDL 133
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 564 LINAGTDCTEEFDAIHSDKAKKMLEDYRIGEL 595

RESULT 10
NIA_CUCMA STANDARD; PRT; 918 AA.
AC P17569;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS Cucurbita maxima (pumpkin) (winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OC NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford N.M., Campbell W.H., Davis R.;
RT "Nitrate reductase from squash: cDNA cloning and nitrate regulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8073-8076(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Hyde G.E., Crawford N.M., Campbell W.H.;
RT "The sequence of squash NADH:nitrate reductase and its relationship
to the sequences of other flavoprotein oxidoreductases. A family of

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RT RT
RL U. Biol. Chem. 266:2342-2347(1991).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -!- SUBUNIT: Homodimer.
CC -!- INDUCTION: By nitrate.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; M33154; AAA33114.1; -.
DR PIR; A41667; A41667.
DR HSSP; P17571; 2CND.
DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR001834; Cyt B5 reductase.
DR InterPro: IPR008335; Euk Mb oxred.
DR InterPro: IPR008333; FAD binding 6.
DR InterPro: IPR001709; FPN_cyt_reductase.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR005066; Mo-co dimer.
DR InterPro: IPR000572; Oxidored molyb.
DR Pfam: PF00970; FAD binding_6; 1.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co dimer; 1.
DR Pfam: PF00175; NAD binding_1; 1.
DR PRINTS: PR00406; CYTB5RDTASE.
DR PRINTS: PR00363; CYTOCHROME5.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; FPNCR.
DR ProDom: PD000612; Cyt B5; 1.
DR PROSITE: PS00191; CYTOCHROME B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
KW METAL 195 195 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 249 249 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 434 434 INTERCHAIN (POTENTIAL).
FT METAL 578 578 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 601 601 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 918 AA; 103383 MW; A2CAFDDADSA1B2D1 CRC64;

Query Match 6.3%; Score 164; DB 1; Length 918;
Best Local Similarity 30.3%; Pred. No. 9.4e-06;
Matches 46; Conservative 22; Mismatches 60; Indels 24; Gaps 6;

QY 3 LVTDLFLNGLTTSKYSVYTH---SVAGNYGPTLKAKKVSAC-----GKTA 46
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 469 LIWLMGMNNCW--FRVKTNMCKPKHGEIGVFEHPTQPGNQSGGMMDRERHLEISTES 526
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 47 GQTLRQSRV---QDKKPGTYSADYASHDRPGDCWMIKVKYDYSRFRADHPGGT-VI 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 527 NQTLK-KSVSTPEMNTASNTYTLSEVKKNSPDSAMIIVGHVYDCTFLKDHPPGGDSI 585
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 STYFGDGTDFVATFHPPAWKQNDYYIGDL 133
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 586 LINAGTDCTEEFDAIHSDKAKKMLEDYRIGEL 617

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NIA2 PHAVU STANDARD; PRT; 890 AA.
ID NIA2 PHAVU STANDARD; PRT; 890 AA.
AC P39866;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).
GN NIA2 OR NR2.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Saxa;
RA Jensen P.E., Hoff T., Stummann S.V., Henningsen K.W.;
ZL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and
CC one molybdenum atom.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U01029; AAA95940.1;
CC PIR; T1805; T11805.
CC HSP; P17571; 2CND.
CC
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Suk_Mb_oxred.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001709; FPN_cyt_reductse.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC InterPro; IPR001433; Oxired_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5REDTASE.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPNCR.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
CC KMOxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
CC Nitrate assimilation; Multigene family.
CC METAL; 165 165 MOLYBDENUM-PTERIN (POTENTIAL).
CC METAL; 219 219 MOLYBDENUM-PTERIN (POTENTIAL).
CC DISULFID; 404 404 INTERCHAIN (POTENTIAL).
CC METAL; 548 548 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC METAL; 571 571 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SEQUENCE 890 AA; 99995 MW; FC3B96F0139DE1E CRC64;
Query Match 6.2%; Score 160; DB 1; Length 890;

Best Local Similarity 30.3%; Pred. No. 2e-05;
Matches 46; Conservative 2; Mismatches 61; Indels 24; Gaps 6;

QY 3 LVTDPLNFLTWSKYSVYTH---SVAGNYGPTLKHAKVSAQ--GKTAGQTLQRSVQD 57
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 439 LIWNLGMWNNCW--FRVKTNVCKEKGEGIVFEHPTQPGNPGCGWMAKEXHLEQS-OE 495
QY 58 KYGP-----TYSLADVASHDRPGDCWMIIVKEKYDISSRRADDPGGT-VI 101
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 496 AKPSLKKSYSTFFMTASKMFSVSEVKHSSPDSAWIIVHGHWYDCTRFKIDHPGGTDSI 555
QY 102 SYTFRGDGTDFATEHPAPAAWKLNDYVIGDL 133
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 556 LINAGTCTCTEEDFAIHSKAKKMWLEIDYRIGEL 587

RESULT 15
FD3E PHAVU STANDARD; PRT; 380 AA.
ID FD3E PHAVU STANDARD; PRT; 380 AA.
AC P32291;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)
DE (Indole-3-acetic acid induced protein ARG1).
GN ARG1.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypocotyl;
RA Yamamoto K.T., Mori H., Imaseki H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata).";
RL Plant Cell Physiol. 33:13-20(1992).
CC -!- FUNCTION: Microsomal (ER) omega-3 fatty acid desaturase introduces
CC the third double bond in the biosynthesis of 18:3 fatty acids,
CC important constituents of plant membranes. It is thought to use
CC cytochrome b5 as an electron donor and to act on fatty acids
CC esterified to phosphatidylcholine and, possibly, other
CC phospholipids.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -!- INDUCTION: By auxin, ethylene and wounding.
CC -!- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D14410; BAA03306.1;
CC PIR; T10898; T10898.
CC InterPro; IPR005804; FA_desat_fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_fam; 2.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC TRANSMEM; 59 78 POTENTIAL.
CC TRANSMEM; 208 231 POTENTIAL.
CC TRANSMEM; 238 256 POTENTIAL.
CC DOMAIN; 97 101 HISTIDINE_BOX-1.
CC DOMAIN; 133 137 HISTIDINE_BOX-2.
CC DOMAIN; 300 304 HISTIDINE_BOX-3.
CC SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;

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Query Match      6.1%; Score 159.5; DB 1; Length 380;
Best Local Similarity 23.0%; Pred. No. 7.4e-06;
Matches 77; Conservative 48; Mismatches 137; Indels 73; Gaps 16;

QY 148 ENRAEFVREGLEFS---SKAWFLLOTLINALEASATATICYDKSYWAIVLSAS---LMG 201
Db 34 DIRAALPKHCWEKSTLRSUSYVLRDLVWVTAASAISFNSW--FFWPLYWPAQGTWFWA 91

QY 202 LFWQCCGWLADHLHQOVFENRTANSFFGYLFGNCVLGFSVSWRTKHNHHTAPN--EC 259
Db 92 LFV-----LCHDCGHSFNSKLSNFVGHILHSLIL--VPYNGWRISHRTHQHNGHVEK 145

QY 260 DEQYTPLEDEDIDPLIIAMSKEILATVESKEILRVLYQYQHYMILPPLLEMARYSW--TFGS 317
Db 146 DESWVPLTE-----KVKKLED--MTRMLRYS--FPPPIFAYPPFYLWNRSPGK 189

QY 318 LLFTFNPDLSSTTKGLIEKGTVAHYWAFSWAAEHILPGVAKPLAWVATELVAG----- 371
Db 190 EGSHEFNPNLSPGGRKGVVTTCLW-----GIV--LSVLLYLSJTGIPIMLK 237

QY 372 -----LLLGFFVFTLSHNGKEVYNBSKDFVRAQV-----ITTRNTRKRGWFNDWF 414
Db 238 LYGVPLYLIFVMWLDFTYLLHHG---YTHKLPWYRGQWSYLRGGLTTVDYDYGWINN-V 293

QY 415 TGGLDTQIEHHLPTMPRENYEKIAPQVEALCKKH 449
Db 294 HEDIGTHVIHHLFPQIPHYHLEVEATKSAKSVLGKY 328

```

Search completed: June 16, 2004, 19:06:19
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:06:22 ; Search time 46 Seconds
(without alignments)
3312.941 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVDFLNFGSTWSKYSV.....AVVKALKEIADASIRLHAH 483

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101741 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREXBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2595	100.0	483	10 Q9LENO	Q9len0 ceratodon p
2	1619	62.4	520	10 Q9LEMO	Q9lem9 ceratodon p
3	1475	56.8	525	10 Q9ZNM2	Q9znw2 physcomitre
4	841.5	32.4	457	3 Q9UVV3	Q9uvv3 mortierella
5	840.5	32.4	457	3 Q8X173	Q8x173 mortierella
6	839.5	32.4	457	3 Q9UVV3	Q9uvv3 mortierella
7	835.5	32.2	457	3 Q9HEV4	Q9hey4 mortierella
8	821.5	31.7	457	3 Q8X174	Q8x174 mortierella
9	821.5	31.7	457	3 Q9HEV1	Q9hey1 mortierella
10	799.5	30.8	477	10 Q8RX80	Q8rx80 phaeodactyl
11	79C	30.4	459	10 Q944W4	Q944w4 pythium irr
12	743.5	28.7	458	3 Q7Z8E2	Q7z8p2 rhizopus sp
13	705.5	27.2	467	3 Q96VC3	Q96vc3 mucor circi
14	668.5	25.8	357	3 Q9HDF4	Q9hdf4 mortierella
15	603.5	23.3	458	10 Q43469	Q43469 helianthus
16	587	22.6	449	10 Q9ZRP7	Q9zrp7 arabidopsis

17	584	22.5	449	10 Q8LB96	Q8lb96 arabidopsis
18	583	22.5	449	10 Q9ZRP8	Q9zrp8 brassica na
19	582.5	22.4	446	10 Q8LLD7	Q8lld7 aquilegia v
20	574	22.1	419	10 Q9SWQ9	Q9swq9 euglena gra
21	574	22.1	448	10 Q04353	Q04353 borago offi
22	574	22.1	453	10 Q84KG8	Q84kg8 primula far
23	573	22.1	448	10 Q9SAU5	Q9sau5 borago offi
24	569.5	21.9	446	10 Q9ZTY9	Q9zty9 ricinus com
25	568	21.9	448	10 Q8VZ22	Q8vzz2 etium gent
26	563	21.7	453	10 Q84KG6	Q84kg6 primula via
27	560	21.6	452	10 Q84KG7	Q84kg7 primula via
28	559	21.5	443	5 Q61388	Q61388 caenorhabdi
29	558	21.5	443	5 Q23221	Q23221 caenorhabdi
30	558	21.5	448	10 Q8VZ21	Q8vzz1 etium pita
31	557	21.5	452	10 Q84KG9	Q84kg9 primula far
32	554.5	21.4	501	4 Q8NCC7	Q8ncc7 homo sapien
33	554.5	21.4	501	4 Q8NCG0	Q8ncg0 homo sapien
34	551	21.2	446	10 Q9FR82	Q9fr82 borago offi
35	550	21.2	444	4 Q96I39	Q96i39 homo sapien
36	550	21.2	444	4 Q96T10	Q96t10 homo sapien
37	549	21.2	444	4 Q60427	Q60427 homo sapien
38	546	21.0	444	4 Q9NRP8	Q9nrp8 homo sapien
39	546	21.0	444	4 Q9NYX1	Q9nyx1 homo sapien
40	535	20.6	444	4 Q96SV3	Q96sv3 homo sapien
41	538.5	20.4	447	11 Q920R3	Q920r3 rattus norv
42	528	20.3	444	4 Q95864	Q95864 homo sapien
43	528	20.3	448	10 Q8L717	Q8l717 argania spi
44	527.5	20.3	447	11 Q920L1	Q920l1 mus musculu
45	526.5	20.3	447	11 Q8VC07	Q8vc07 mus musculu

ALIGNMENTS

RESULT 1

Q9LENC PRELIMINARY; PRT; 483 AA.
ID Q9LENO
AC Q9LENO;
DT C1-OCT-2000 (TREMBLrel. 15, Created)
DT C1-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB Delta 6-fatty acetylase.
OS Ceratodon purpureus (Moss).
OC Eukaryota, Viridiplantae; Streptophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt3; TISSUE=Protonemata;
EX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Garke T., Zaehring U., Stymne S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily.";
RT Eur. J. Biochem. 267:3801-3811(2000).
RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL; AJ250734; CAB94992.1; -;
DR HSSP; P34166; IBSM.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat. fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 483 AA; 54857 MW; C451D042169A1C2 CRC64;

Query Match 100.0%; Score 2595; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 5.4e-217;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALVTDLFLNGLTWSKYSVYTHSYAGNYGPTLKHAKKVSQAQKTAGTQLRQSRVQDKP 60
DB 1 MALVTDLFLNGLTWSKYSVYTHSYAGNYGPTLKHAKKVSQAQKTAGTQLRQSRVQDKP 60
QY 61 GTYSADVASHDRPGDCWMIKVKYVDISRFDHGGTIVSYFGRDGDVDFATHPPA 120
DB 61 GTYSADVASHDRPGDCWMIKVKYVDISRFDHGGTIVSYFGRDGDVDFATHPPA 120
QY 121 AKQMLNDYIGDLARBEPLDELLKDYRDMRAEFVREGLFKSSKAWFLQTLINAALEAAS 180
DB 121 AKQMLNDYIGDLARBEPLDELLKDYRDMRAEFVREGLFKSSKAWFLQTLINAALEAAS 180
QY 181 IATICYDKSWAIVLSASLGLFVQCGMLAHDFLHQVFNENTANSFFGYLFGNCVLGF 240
DB 181 IATICYDKSWAIVLSASLGLFVQCGMLAHDFLHQVFNENTANSFFGYLFGNCVLGF 240
QY 241 SVSWMTKNIHHTAPNECEDQVTPLEDIDITPLIATWSKEIILATVESKRLRLVLOVQHY 300
DB 241 SVSWMTKNIHHTAPNECEDQVTPLEDIDITPLIATWSKEIILATVESKRLRLVLOVQHY 300
QY 301 MILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHYAWFSAWAFHILPGVAKPL 360
DB 301 MILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHYAWFSAWAFHILPGVAKPL 360
QY 361 ANMVATELVAGLLGVFTLSHNGKEVYNESKDFVRAQVITTRTKRGWENDMTGGTLD 420
DB 361 ANMVATELVAGLLGVFTLSHNGKEVYNESKDFVRAQVITTRTKRGWENDMTGGTLD 420
QY 421 QISHHLFPTMPRNYPKIAPQVEALCKKHGLEVDNVSUWGSVAUVKALKEIADASIRL 480
DB 421 QISHHLFPTMPRNYPKIAPQVEALCKKHGLEVDNVSUWGSVAUVKALKEIADASIRL 480
QY 481 HAH 483
DB 481 HAH 483

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RESULT 2

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Q9LEM9 PRELIMINARY; PRT; 520 AA.
AC Q9LEM9;
DT 01-OCT-2000 (T-REMS:rel. 15, Created);
DT 01-OCT-2000 (T-REMS:rel. 15, Last sequence update);
DE Delta 6-fatty acid desaturase.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicrotriales; Dicrotraceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt3; TISSUE=Protonemata;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehring U., Stymme S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily.";
RL Eur. J. Biochem. 267:3801-3811(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ250735; CAB94993.1; -.
DR HSPSP; P00171; IREB.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;

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Query Match 62.4%; Score 1619; DB 10; Length 520;

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Best Local Similarity 61.5%; Pred. No. 4.8e-132;
Matches 302; Conservative 72; Mismatches 101; Indels 16; Gaps 3;

QY 1 MALVTDLFLNGLTWSKYSVYTHSYAGNYGPTLKHAKKVSQAQKTAGTQLRQSRVQDKP 60
DB 25 MPLVSDFLNGLTGLGWSLST-TFAKRLTTKSHSSDISVEAQKESVARGPVENISQSV 83
QY 47 GQTLRQSRVQDKPGKGYSLADVASHDPRPGDCWMIKVKYVDISRFDHGGTIVSYFGR 106
DB 84 AQPIRRRWQDKPGKGYSLADVASHDPRPGDCWMIKVKYVDISRFDHGGTIVSYFGR 143
QY 107 RQGTDFVAFHFAAKQMLNDYIGDLARBEPLDELLKDYRDMRAEFVREGLFKSSKAWF 166
DB 144 RDATDFVSTFHAATSWKILQNFYIGNLVREPTLELLKEYRELKALFRLQFLKSSKSIY 203
QY 167 LLQTLINAALEAASIAATICYDKSWAIVLSASLGLFVQCGMLAHDFLHQVFNENTAN 226
DB 204 LFKTLINVSIVATISIAIISLYKSYRAVLLSASLGLFVQCGMLSHDFLHQVFNENTAN 263
QY 227 SFFGYLFGNCVLGFSVSWMTKNIHHTAPNECEDQVTPLEDIDITPLIATWSKEIILATV 286
DB 264 DVGVYVGVNVLGFSVSWMTKNIHHTAPNECEDQVTPLEDIDITPLIATWSKEIILATV 323
QY 287 ESKRIERLVLOYQHYMILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHYAWFS 346
DB 324 ESKTMRVLVLOVQHYMILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHYAWFS 383
QY 347 WAAFHILPGVAKPLAMVATELVAGLLGVFTLSHNGKEVYNESKDFVRAQVITTRTK 406
DB 384 SVAFYLLPG-WKPVWVWVSELXSGFLGVFVLSHNGMEVYNESKDFVRAQVITTRTK 442
QY 407 RGFNDWFTGGTLDITQIEHHLFPTMPRNYPKIAPQVEALCKKHGLEVDNVSUWGSVAUV 466
DB 443 AGVNDWFTGGTLDITQIEHHLFPTMPRNYPKIAPQVEALCKKHGLEVDNVSUWGSVAUV 502
QY 467 KALKEIADAS 477
DB 503 KTLKQVADAAS 513

RESULT 3
Q9ZNN2 PRELIMINARY; PRT; 525 AA.
AC Q9ZNN2;
DT 01-MAY-1999 (T-REMS:rel. 10, Created);
DT 01-MAY-1999 (T-REMS:rel. 10, Last sequence update);
DT 01-JUN-2003 (T-REMS:rel. 24, Last annotation update);
DE DELTA6-acyl-lipid desaturase.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEDW. B. S. G;
RX MEDLINE=98416756; PubMed=9744093;
RA Girke T., Schmidt H., Zaehring U., Reski R., Heinz E.;
RT "Identification of a novel delta 6-acyl-group desaturase by targeted
RT gene disruption in Physcomitrella patens.";
RL Plant J. 15:39-48(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ222981; CAAL1033.1; -.
DR EMBL; AJ222980; CAAL1032.1; -.
DR HSPSP; P04166; IICC.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

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KW Heme.
SQ SEQUENCE 525 AA; 59369 MW; 530F158B0C97C83F CRC64;

Query Match 56.8%; Score 1475; DB 10; Length 525;
Best Local Similarity 55.3%; Pred. No. 1.7e-119;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6

QY 1 MALVTDFLNFELGTT---WSKYSVYVTHSVAGNYGPTLKHAKVVS----- 40
Db 25 MSILFFDFSYVSTVGWSVHSIQLK-----RLTSKRRVSSAAVQCISAEVORNSS 77
QY 41 -----ACGCTAGTGTLRORSVODKKPGTYSIADVAASHDRPGCWMIKEKVYDISRFADD 94
Db 78 TQGTAEALAESVVKPTRRRSQWK-SHPPLSEVAVENKPSDCWIVVKVYDVSNFADE 136
QY 95 HPGGTVTISTYGRDGTDFATFHPPAWKQINDYTGGLAREEPDELLELLKYDRMKRAFTV 154
Db 137 HPGGSVLISTYGRDGTDFVSSFHAASTWKILQDFYIGSVVERVEPTPELLKDFREMRALFL 196
QY 155 REGEPKSKAMFLQTLINAAALFAASIAITICVDKSYWAIVLASLGLFVQCQGLAHDF 214
Db 197 REQPLKSKSLYVWKLLTNVALFAASIAIICWSKTIISAVLASACMWALCFQCQGLSHDF 256
QY 215 LHQOVFNRTANSFGYLFQNCVLGFSVSWRTKNIHHHTAPNECDEQYTPLEDDIDITLP 274
Db 257 LHNQVFTRWLNEVGVYVIGNAVLGFSTGWWKEKINLHHAANECDQYQPIDEIDITLP 316
QY 275 IIAWSKEILATVESKRILRVLYQYQHMYLPLLFPMARYSWTFCGLFTENPDLSTTKGITE 334
Db 317 LIAWSKILATVENKTELRIILYQHLFPMGLLFFARGSLFWSTWYTSVAVLSPVDRLL 376
QY 335 KGTVAHYVAFWSAAFHLLPGVAKPLAMVATLWAGLLGLVFTLSNGKEVYVNESKDF 394
Db 377 KGTVLHFYFWEVGTACYLLPG-WKPLVWMAVTELMSGMLLGLFVFLSHNGMEVYVNSSKEF 435
QY 395 VRAQVITTRNTKRGWENDWFTGGDLDTQTEHHLFPTMPRHNYPKIAPOVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDLKGINFDWFTGGLNRQLEHHLFPTMPRHNLNKIAPRVEVFCCKHGLYVE 495
QY 455 NVSVVGASVAVVKALKEIADASIRLHA 492
Db 496 DVSIATGTCKVLKALKEVA-EAAAPQHA 522

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RESULT 4
Q9UVV3
ID Q9UVV3 PRELIMINARY; PRT; 457 AA.
AC Q9UVV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Delta-6 fatty acid desaturase.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC3221;
RC MEDLINE=99406036; PubMed=10478922;
RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chao G.-M., Kirchner S.-J., Mukerji P., Knutzen D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."
RL Lipids 34:649-659(1999).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL; AF110510; AAF08683.1; -.
DR HSSP; P04166; 1EUE.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cy-B5.
DR InterPro; IPR005804; FA desat fam.
DR Pfam; PF00487; FA desaturase; 1.

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DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA Desat fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51837 MW; D90169E86911450A CEC64;

Query Match 32.4%; Score 841.5; DB 3; Length 457;
Best Local Similarity 39.2%; Pred. No. 1.8e-64;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10

QY 62 TYSADV-----ASHDRPDCMWIVKEKVDISRFADHPDGGTGVISTVTFGRDGTDFV 113
DB 9 TFTAENVLREALNEGKDAEAPFLMIDNKVYDVREFPVDPHGGSVLTHVGKDGTDV 68

QY 114 ATTFPPAAKOLNDYYIGDL---ARESPDELLKDYRDMRAEFVREGLFKSKAWFLQ 170
DB 69 DTFPEPAHWETLANFYGDIDESDROIKNDFAAEVKRLTLFQSLGYDSSKAYAFKV 128

QY 171 LINAALFAASTATICY--DKSYWAIVTSASLMGLFVQCGGLAHDFLHQOVFNRTANSF 228
DB 129 SFNLICINGLSIVIAKNGQTSTLANVLSALLGLFVQCGGLAHDFLHHQVFPQDRFWGDL 188

QY 229 EGYLFGNCVLGFSVSWRTKNIHHITAPNECDQYTPDDEIDILPIIAISK--ELLAT 285
DB 199 FGAFGLGVYCGQFSSSWKDKINTHAAPNVAGE-----DPDIDTHPLLTMSEHALEMFS 243

QY 286 VESKRILRVLYQYHML-----PLLFMARYSWTGLSLFTNPULSTTK----- 330
DB 244 VPDEELTRM--WSRFMLNQTMWTFPPLISFARLSWCLQSILFVL-PNQAHKPSGARVPI 300

QY 331 GLIEKGTVAEHYAWFSWAAZHLPGVAKPLAMWATELVAGLLGLGVFTLSHGKEVYNE 390
DB 301 SLVEQLSLAHWTYLAITMELFKDPVNMVLYFLVSQAVCGNLLAIVFSLNENGMFVISK 360

QY 391 SK----DFVRAQVITTRTKGNWDFGTGLDTQIEHLEPTWPRHNYKPIAPOVEALC 446
DB 361 BEAVDMDFTKIITGRDVPGLFANFTGGLNYQIEHLLFSPMRHNFPSKIQPAVETLC 420

QY 447 KKHGLEVDNVSWGASVAVVKALKEIADEAS 477
DB 421 KKINVRVHTTGIEGTAEVFSRLNEVSKAAS 451

RESULT 5
Q8X173 PRELIMINARY; PRT; 457 AA.
AC Q8X173
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Delta 6 fatty acid desaturase.
GN G1560.
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsis.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6-22;
RA Xing L., Liu L., Li M., Hu G.;
RT "Cloning and sequence analysis of the delta 6 fatty acid desaturase
RT gene from Mortierella isabellina M6-22 genomic and cDNA";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AF465282; AAL73948.1; -
GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_Desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.

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DR ProDom: PD001081; FA desat fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51784 MW; 78CE779CE9E28A CRC64;

Query Match 32.4%; Score 840.5; DB 3; Length 457;
Best Local Similarity 40.4%; Pred. No. 2.1e-64;
Matches 172; Conservative 70; Mismatches 149; Indels 35; Gaps 9;

QY 79 MIWKEVYDISRADDHPGTVISTYFGRDGTDFATFHPPAWKQLNDYYIGDLAREEP 138
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 93
34 MIIDNKVYDVREFVDPHPGSSVILTHVGKGTDFDTFHPPEAAWETLANEYVGDIDESDR 93
QY 139 L---DELLKDYRDVRAEFVREGLFKSKAWFLQTLINAALEFAASTATICY--DKSYWAI 193
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 153
94 AIKNDPFAAEVRKRLTLFQSLGYDSSKAYAFKVSFNLGICWGLSTFIVAKWGQSTLAN 153
QY 194 VLSASLGLFVQCCGWLADHFLFQQVFNKNTANSFFGLFCNCVLFGSVSWRTKNIHH 253
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 213
154 VLSAALLGLFWQCCGWLADHFLFHHQVFDQRFWGDLFCAFLGGVCGGFSSSWKKKNIHH 213
QY 254 TAPNECEQVTPDEDIDTLPILANSK---EILATVESKRLILVLOQHYMIL----- 303
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 266
214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSVPDELTRM--WSRFVNLQNTWYF 266
QY 304 PLLFMARYSWTFGLLFTFNPDLSTTK-----GLIEKGTVAHFYAWFSWAAPHILPG 355
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 325
267 PILSFARLSWCLQSILFVL-PNGQAHKPSGARVPISLVEQLSLAHVHTWYLAITMFLFKD 325
QY 356 VAKPLAMVATELVAGLLGFVFTLSHGKVEYNESK-----DFVRAQVITTRNTKRGWEN 411
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 385
326 PVNMVYFLVSQAVCGNLLAIVFSLNENGMFVSKKEAVDMDFTKQIITGRDVHPGLFA 385
QY 412 DWFTGGDLOIEHLLFTMPRHNPYKPIAPOVEALCKKHGLEVDNVVVGASVAVVKALKE 471
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 445
386 NWFTGGNYQIEHLLFSPMRHNSKIQAVETLCKKYGVRHYHTGMIEGTAEVFSRLNE 445
QY 472 IADEAS 477
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 446 VSKAAS 451

RESULT 6
Q9UYV3 PRELIMINARY; PRT; 457 AA.
ID Q9UYV3
AC Q9UYV3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Delta-6 fatty acid desaturase.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1S-4;
RX MEDLINE=20035749; PubMed=10570972;
RA Sakurada E., Kobayashi M., Shimizu S.;
RT "Delta 6-Fatty acid desaturase from an arachidonic acid-producing
RT Mortierella fungus. Gene cloning and its heterologous expression in a
RT fungus, Aspergillus.";
RL Gepe 238:445-453 (1999).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR HSSP; P04166; IEUE.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA desat fam.
DR ProDom; PD001081; FA desat fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.

DR ProDom: PD001081; FA desat fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51816 MW; 5C4B3D7312439543 CRC64;

Query Match 32.4%; Score 839.5; DB 3; Length 457;
Best Local Similarity 40.1%; Pred. No. 2.6e-64;
Matches 171; Conservative 71; Mismatches 149; Indels 35; Gaps 9;

QY 79 MIWKEVYDISRADDHPGTVISTYFGRDGTDFATFHPPAWKQLNDYYIGDLAREEP 138
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 93
34 MIIDNKVYDVREFVDPHPGSSVILTHVGKGTDFDTFHPPEAAWETLANEYVGDIDESDR 93
QY 139 L---DELLKDYRDVRAEFVREGLFKSKAWFLQTLINAALEFAASTATICY--DKSYWAI 193
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 153
94 AIKNDPFAAEVRKRLTLFQSLGYDSSKAYAFKVSFNLGICWGLSTFIVAKWGQSTLAN 153
QY 194 VLSASLGLFVQCCGWLADHFLFQQVFNKNTANSFFGLFCNCVLFGSVSWRTKNIHH 253
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 213
154 VLSAALLGLFWQCCGWLADHFLFHHQVFDQRFWGDLFCAFLGGVCGGFSSSWKKKNIHH 213
QY 254 TAPNECEQVTPDEDIDTLPILANSK---EILATVESKRLILVLOQHYMIL----- 303
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 266
214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSVPDELTRM--WSRFVNLQNTWYF 266
QY 304 PLLFMARYSWTFGLLFTFNPDLSTTK-----GLIEKGTVAHFYAWFSWAAPHILPG 355
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 325
267 PILSFARLSWCLQSILFVL-PNGQAHKPSGARVPISLVEQLSLAHVHTWYLAITMFLFKD 325
QY 356 VAKPLAMVATELVAGLLGFVFTLSHGKVEYNESK-----DFVRAQVITTRNTKRGWEN 411
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 385
326 PVNMVYFLVSQAVCGNLLAIVFSLNENGMFVSKKEAVDMDFTKQIITGRDVHPGLFA 385
QY 412 DWFTGGDLOIEHLLFTMPRHNPYKPIAPOVEALCKKHGLEVDNVVVGASVAVVKALKE 471
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 445
386 NWFTGGNYQIEHLLFSPMRHNSKIQAVETLCKKYGVRHYHTGMIEGTAEVFSRLNE 445
QY 472 IADEAS 477
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 446 VSKAAS 451

RESULT 7
Q9HEY4 PRELIMINARY; PRT; 457 AA.
ID Q9HEY4
AC Q9HEY4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Delta-6 fatty acid desaturase.
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsis.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RC Ming-Chan L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
RT from Mortierella isabellina.";
RL Junwu Xitong 0:0-0 (2001).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR HSSP; P04166; IEUE.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00487; FA desat fam.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.

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KW Heme.
 SQ SEQUENCE 457 AA; 51772 MW; 868E7EB21172D5AF CRC64;
 Query Match 32.2%; Score 835.5; DB 3; Length 457;
 Best Local Similarity 40.1%; Pred. No. 5.8e-64;
 Matches 171; Conservative 70; Mismatches 150; Indels 35; Gaps 9;
 QY 79 MIVKEKYDISRFADDPGGTIVISTYFGRDGTDFATFHPPAWKQLNDYVIGDLAREEP 138
 Db 34 MIIDNKVYDREFVDPDHPGGSVILTHVGKGDVDFTFHPPEAAWETLANFYVGDIDESDR 93
 QY 139 L---DELLKYDRMAEFVREGLEKSKAWFLQTLINAAALFAASIATICY--DKSYWAI 193
 Db 94 AIKNDDEFAAEVRKLTLPQSLGYDSSKAYAFKVSFNLCTWGLSTFIVAKWGQTSTLAN 153
 QY 194 VLSASLMGLFVQCCGLAHDFLHQVFNRTANSEFFGYLFGNCVLGFSVSWRTKHNTHH 253
 Db 154 VLSAALLGLFWQCGWLADFLHHQVQDRFWGDLFGAFLGGVCGQFSSSWWKDKHNTHH 213
 QY 254 TAPNECDQYTPLEDIDITLPIIAWSK---ELATVSKRLRLVLOYQHYML----- 303
 Db 214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSVDPDEELTRM--WSRFVNLQTFYF 266
 QY 304 PLLFMARYSWTFGSLITFTNPDLSTTK-----GLIEKTVAFHYAFWAFSMAAFELPG 355
 Db 267 PILSPARLSWCLQSILVL-PNGQAHKPSGARVPSILVEQLSLAMHWTWYLATMFLFIKD 325
 QY 356 VAKPLAWVATELVAGLLGFVFTLSHGKEVYNESK----DFVRAQVITTRNTKRGWEN 411
 Db 326 PVNMVYELVSQVCGNLLAIVFSLNHNMPVISKEEAVDMDFFTKQIITGRDHPGLFA 385
 QY 412 DWFTGGDLDTQIEHLFPTMPRHNPYKIPQVEALCKKHGLEVDNVSVVGASVAVVKALKE 471
 Db 386 NWFTGGLNYQTEHHLFPTMPRHNPFSKIQPAVELTCKKYGVRYHTTGMIEGTAEVFSRLNE 445
 QY 472 IADBAS 477
 Db 446 VSKAAS 451

RESULT 8

Q8X174
 ID Q8X174 PRELIMINARY; PRT: 457 AA.
 AC Q8X174
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Delta 6 fatty acid desaturase.
 GN GLD6D.
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
 OC Mortierellaceae; Mortierella.
 CX NCBI_TaxID=64518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 16266;
 RA Liu L., Li M., Hu G., Xing L.;
 RT "Cloning and sequence analysis of the delta 6 fatty acid desaturase
 gene from Mortierella alpina ATCC16266 genomic and cDNA."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF465281; AAL73947.1; -
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA desat fam; 2.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 457 AA; 51915 MW; 087B91DC47F2EDA3 CRC64;

RESULT 9

Q9HEY1
 ID Q9HEY1 PRELIMINARY; PRT: 457 AA.
 AC Q9HEY1
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Delta 6-fatty acid desaturase.
 GN GLD6D-I.
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
 OC Mortierellaceae; Mortierella.
 CX NCBI_TaxID=64518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 16266;
 RA Liu L., Li M., Hu G., Xing L.;
 RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
 in Saccharomyces cerevisiae."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF307940; AAG45092.1; -
 DR EMBL; AP465283; AAL73949.1; -
 DR HSRP; P04166; 1E0E.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.

QY 162 SKAWFL--LQTLINAALFAASIIATICYDKSYNAIVLSASLNGLFVQCGWLAHDFHQV 219
 Db 130 STCFYIYKVTLLVCIAGLAKWGBSTLAVFAASLVGLFWQCGWLAHYAHQV 189
 QY 220 FENRTANSFGYLGNCVGFVSVMWRTKNIHHTAPNECDEQYTLDEIDTLPILAWS 279
 Db 190 IKDPNVNLFVTFGNLVQGSLSWKNKENTHASTNSVGE-----DPDIDTAPILLWD 244
 QY 280 KETLATVESK-----RIL--RVLYOYHYMLPLLFWMARYSWTFGSLFTF--NPDL 327
 Db 245 EFANVYGLSKDKAGDFRFAIEHILPYOTRYFFILGPARISWALQSIYFKEINLN 304
 QY 328 TTKGL--LEKGVAFHYAFSNAAPHILPGVAKPLAMVATLWAGLLGLGFVFTLSHGK 385
 Db 305 KSKLLSKCERIF--VHWVFYCTIAWISSIRNIAMFFVVSQITGTYLLAIVFAMNHGM 364
 QY 386 EYVNESK-----DFVRAQVITTRTKGWFNDWFTGGLDQIEHELEPTMREHNPYKAPQ 441
 Db 365 PYSPEANHTFELYLCITGRDNCVTFGDLWMLGGLNYQIEHELEFEMPFRHLSKVSM 424
 QY 442 VEALCKKHGLEYNWSVVGASVAVKAL 469
 Db 425 VKELAQKYNIPYHDTTIVIGTIEVLQTL 452

RESULT 14

Q9HDF4
 ID Q9HDF4 PRELIMINARY; PRT; 357 AA.
 AC Q9HDF4
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Delta 6-fatty acid desaturase (fragment).
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
 OC Mortierellaceae; Mortierella.
 OX NCBI_TaxID=64518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA King L., Li M., Liu L., Hu G.;
 RT "Cloning and sequence analysis of the conserved region of delta 6-
 fatty acid desaturase gene from Mortierella alpina."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA King L., Li M., Liu L., Hu G., Zhang L.;
 RT "Cloning and sequence analysis of the conserved region of delta 6-
 fatty acid desaturase gene from Mortierella alpina."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307942; AAG45094.1; -.
 DR EMBL; AF307941; AAG45093.1; -.
 DR HSSP; P04166; 1RJE.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR ProSITE; PS00191; CYTOCHROME B5_1; 1.
 DR ProSITE; PS50255; CYTOCHROME_B5_2; 1.
 FT NON_TER 1
 FT NON_TER 357
 SQ SEQUENCE 357 AA; 40796 MW; C8D9CE1283BB1688 CRC64;

Query Match 25.88; Score 668.5; DB 3; Length 357;
 Best Local Similarity 39.28; Pred. No. 1.4e-49;
 Matches 143; Conservative 59; Mismatches 128; Indels 35; Gaps 9;
 QY 91 FADHPGCGTISTYFGDGTGFATFHPAAWKLQNDYIGTLAREEPL---DELLKDYR 147
 Db 1 FVDPHFGSVILTHVGKDGTVDFTFHPEAAWETLANFYVGCIDESDRAIKNDFFAAEVR 60

QY 148 DMRAEFVREGLFSSKAWFLQTLINAALFAASIIATICY--DKSYNAIVLSASLNGLFVQ 205
 Db 61 KLRTLFQSLGYDDSKAYAFKVSFNLICWGLSTFIVAKRGQTSTLANELSAALLGLFWQ 120
 QY 206 QCWLHADFHQVFNENRTANSFGYLGNCVGFVSVMWRTKNIHHTAPNECDEQYTP 265
 Db 121 QRCWLHADFHQVFNENRTANSFGYLGNCVGFVSVMWRTKNIHHTAPNECDEQYTP 176
 QY 266 LDDSDIDTLPILAWSK-----EILATVESKRIILRVLYOYHYML-----PLLFMARYSWTF 315
 Db 177 -DPDIDTLPILAWSK-----EILATVESKRIILRVLYOYHYML-----PLLFMARYSWTF 233
 QY 316 GSLETFNPDLSTTK-----GLIEKGVAFHYAFSNAAPHILPGVAKPLAMVATE 367
 Db 234 QSILFVL--PNCQAKHPSGARVPISLVEQLSLAMHWTWYLATMFLFKDPVNMVYFLVSQ 292
 QY 368 LVAGLLGLGFVFTLSHGKVEYVNESK-----DFVRAQVITTRTKGWFNDWFTGGLDQIE 423
 Db 293 AVCNLLAIVLSLHNGMPVISKEEAVDMDFFIKQIITGRDVEHPELFAFWFTGGLNQIE 352
 QY 424 HLLFP 428
 Db 353 HLLFP 357

RESULT 15
 Q43469
 ID Q43469 PRELIMINARY; PRT; 458 AA.
 AC Q43469
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 GN SLD1.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
 OC Helianthus.
 OX NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. inbred line HA89;
 RC TISSUE=cotyledons of developing sunflower fruits;
 RX MEDLINE=96028121; PubMed=7588718;
 RA Sperling P., Schmidt H., Heinz E.;
 RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
 desaturases."
 RL Eur. J. Biochem. 232:798-805(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. inbred line HA89;
 RC TISSUE=cotyledons of developing sunflower fruits;
 RX MEDLINE=21116801; PubMed=11171153;
 RA Sperling P., Blume A., Zaehring U., Heinz E.;
 RT "Further characterization of delta 8-sphingolipid desaturases from
 higher plants."
 RL Biochem. Soc. Trans. 28:638-641(2000).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; X87143; CAA60621.1; -.
 DR EMBL; S68358; S68358.
 DR HSP; P00171; 1F03.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR ProSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E99245 CRC64;

Query Match		23.3%;	Score 603.5;	DB 10;	Length 456;
Best Local Similarity		31.1%;	Pred. No. 8.9e-44;		
Matches 136;		Conservative 85;	Xismatches 193;	Indels 23;	Gaps 8;
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Db	11	SIADGKKVIIS-KELKHNNDNDLWISILGVYVTEWAKEHPGDAPLINLAGQDVDA	69		
Qy	113	FATHPFAAMKQLNDYYIGDLAREEPIDELLKDYRDMRAEFVREGLFKSSKAWELLQTLI	172		
Db	70	FIACHPGTAWKHLKLTGYHLKQVQSDISRDYKKLASEFAKAGMPEKKGHVIYSLCF	129		
Qy	173	NAALFAASIATICDKSYWAIVLSASLMLFVQCCGMLAHDFLHQOVFENRTANSFFCYL	232		
Db	130	VSLLSACVYGVLYSGSFHMLSGAILGLAWMQIAYLGHDAHYQMMATRGWNKFAGIF	189		
Qy	233	PGNCVLGFSVSWRTTKNHHHTAPNECDEQVTPLEDEDITLPTIAWSKEILATVESKRIL	292		
Db	190	IGNCITGISIAWKKWTHNAHHIACNSLD-----YDPLOHLPLAVSSKLFNSITSVFG	244		
Qy	293	RVL-----QYQHYMILPLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAHY	342		
Db	245	RLTFDPLAREFFVSQYLYYPIMCVARVNLVLOTIELLISKRKIPDRGLNLGLTF-W	303		
Qy	343	AWFSWAAPHILPGVAKPLAWVATELVAGLLLGFWFTLSHNGKEYV---NESKDFVRAQV	399		
Db	304	TFPFLVSR-LPNWPERVAFVLVFCVTG-IGHQFTLNHFSGDYVVGPPKGDNNWFEKQT	361		
Qy	400	ITTRNKRGFNDWFTGGLDTQIEHHLFPTWPRHNYPKIAPQVEALCKKHGLEYNVSWV	459		
Db	362	RGTDIACSSWMDWFFGSLQFQLEHHLFRLPRCHLSISPICRELCKKYNLPYVLSLSPY	421		
Qy	460	GASYAVVVKALKEIADEA	476		
Db	422	DANVTTLKTLRTAALQA	438		

Search completed: June 16, 2004, 19:10:42
Job time : 49 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2004, 02:36:30 ; Search time 3746 Seconds
(without alignments)
3850.356 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFNLFLGTWTSKYSV.....AVKALKEIADERSIRLHAH 483

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09980468/runat.16062004.174742.27187/app.query.fasta.1.647
-DB=EST -QFWT=fastcap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09980468 -CGN 1 1 3437 @runat.16062004.174742.27187 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: em_estba:*
2: em_esthum:*
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4: em_estma:*
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6: em_estpi:*
7: em_estro:*
8: em_estt:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
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16: em_eston:*
17: em_gss_hum:*
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20: em_gss_vit:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	652	25.1	753	12	BJ579910	BJ579910 BJ579910
C 2	649	25.0	764	12	BJ169984	BJ169984 BJ169984
C 3	634	24.4	688	12	BJ170744	BJ170744 BJ170744
C 4	617	23.8	728	12	BJ597842	BJ597842 BJ597842
C 5	583	22.5	697	12	BJ599570	BJ599570 BJ599570
C 6	583	22.5	698	12	BJ604593	BJ604593 BJ604593
C 7	567.5	21.9	1764	11	AV103762	AV103762 Zea mays
C 8	539	20.8	519	12	BQ040185	BQ040185 gdl2ell.y
C 9	529	20.4	2272	11	AK076485	AK076485 Mus muscu
C 10	528	20.3	1335	29	AY418548	AY418548 Homo sapi
C 11	527.5	20.3	3318	11	AK083959	AK083959 Mus muscu
C 12	517	19.9	622	10	AW476747	AW476747 ga37d12.y
C 13	516	19.9	1689	11	AK080414	AK080414 Mus muscu
C 14	514	19.8	3129	11	AK029318	AK029318 Mus muscu
C 15	503	19.4	1335	29	AY418550	AY418550 Mus muscu
C 16	499	19.2	746	12	BJ583356	BJ583356 BJ583356
C 17	479	18.5	766	12	BJ600861	BJ600861 BJ600861
C 18	478	18.4	3697	11	AK090042	AK090042 Mus muscu
C 19	443.5	17.1	699	12	BJ597953	BJ597953 BJ597953
C 20	443.5	17.1	700	12	BJ599342	BJ599342 BJ599342
C 21	443.5	17.1	726	12	BJ603698	BJ603698 BJ603698
C 22	441.5	17.0	1131	29	AY420234	AY420234 Homo sapi
C 23	439	16.9	2862	11	AK083282	AK083282 Mus muscu
C 24	438	16.9	480	12	BJ599078	BJ599078 BJ599078
C 25	428.5	16.5	1131	29	AY420236	AY420236 Mus muscu
C 26	409	15.8	522	12	BJ601553	BJ601553 BJ601553
C 27	409	15.8	985	14	CB264523	CB264523 55-B02082
C 28	401.5	15.5	1079	29	AY420235	AY420235 Pan trogl
C 29	392.5	15.1	507	12	BJ173747	BJ173747 BJ173747
C 30	382	14.7	867	29	CG847823	CG847823 ZM88B031
C 31	377	14.5	721	13	BQ864828	BQ864828 QGC37M12
C 32	376	14.5	696	13	BQ861565	BQ861565 QGC18P18
C 33	375	14.5	786	14	CB837141	CB837141 BN45_051D
C 34	373.5	14.4	721	14	CB972537	CB972537 CAB3000L
C 35	370.5	14.3	934	29	CG264539	CG264539 GWMGP72TV
C 36	368	14.2	748	13	BQ976973	BQ976973 QH123104
C 37	367.5	14.2	817	14	CB893839	CB893839 EST646631
C 38	366	14.1	756	13	BU025934	BU025934 QHG12E03
C 39	364.5	14.0	651	13	BQ409001	BQ409001 GA_Ed001
C 40	364.5	14.0	914	29	CG463170	CG463170 PUTP24TD
C 41	363	14.0	922	29	CG238209	CG238209 OG08216TV
C 42	361	13.9	655	13	BU026750	BU026750 QHG17020
C 43	359	13.8	745	13	BU026884	BU026884 QHG18G02
C 44	359	13.8	765	13	BU024179	BU024179 QHF16J23
C 45	357.5	13.8	427	10	AW699009	AW699009 gb20d09.y

ALIGNMENTS

RESULT 1
BJ579910/C
LOCUS BJ579910
DEFINITION BJ579910 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens cDNA clone pttb12117 3', mRNA sequence.
ACCESSION BJ579910
VERSION BJ579910.1
KEYWORDS EST, Physcomitrella patens subsp. patens
SOURCE Physcomitrella patens subsp. patens
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Bryopsida; Funariidae; Funariaceae; Physcomitrella.

Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp/>).

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FEATURES
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            /clone_lib="full length cDNA library, chloronemata and young gametophores"

ORIGIN
Alignment Scores:
Pred. No.:      5,91e-68      Length:      764
Score:          649.00      Matches:    127
Percent Similarity: 73.56%      Conservative: 26
Best Local Similarity: 61.06%      Mismatches: 53
Query Match:    25.01%      Indels:     2
DB:              12      Gaps:         2

US-09-980-468-2 (1-483) x BJ169984 (1-764)

QY 275 IlelleAlaTrpSerLysGluLeuAlaThrValGluSerLysArgIleLeuArgVal 294
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QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr 314
Db 702 CTCCTATACAGCATCTGTTCTTCATGGGCTGCTATTTTTCGCCGCTGGTAGTGGCTC 643
QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuLeuGlu 334
Db 642 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCTCACTGTGCGACAGGTTGTGGAG 583
QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 582 AAGGGAACCTGTTCTGTTTCACTACTTTTGGTTCTGTCGGGACAGGCTATCTCTCCCT 523
QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
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QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
Db 466 GCGTTTGTATTCTACTTAGCCCAATGGGATGGAGGTTTATATTCGTCTAAGAATTC 406
QY 395 ValArgAlaGlnValIleThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 405 GTGAGTGCACAGATCGTATCCACCGGATATCAAGGAAACATATTCAACGACTGGTTC 346
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisGlyLeuPheProThrMetProArgHisAsn 434
Db 345 ACTGTGTGGCTTAACAGGCAATAGAGCATCATCTTTTCCCACAATATGCCAGGCATATAT 286
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 285 TTAACAAAATAGCACCTAGATGGAGGTCTTCTGTAAAGAACACGCTCTGGTGTAGCAA 226
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGlyIleAlaAsp 474
Db 225 GAGGTATCTATCTCTACCGGCATCTGCAAGGTTTGAAGCATTTGAAGAGTGGCG--- 169
QY 475 GluAlaSerIleArgLeuHisAla 482
Db 168 GAGGCTGGCGCAGCAGCATGCT 145

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RESULT 3 BJ170744/c LOCUS DEFINITION

BJ170744 688 bp mRNA linear EST 16-OCT-2003
gametophores Physcomitrella patens subsp. patens cDNA clone
pph26120 3', mRNA sequence.
BJ170744
BJ170744 GI:18338720

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariaceae; Physcomitrella.
1. (bases 1 to 688)
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohata, Y. and Hasebe, M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
12808149
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
E-mail: tshini@genes.nig.ac.jp

JOURNAL MEDLINE PUBMED COMMENT

A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector (5'- GAGAGAGAGAGATCCACCTGGAGAGTTTTTTTTTTTNN-3' was
used as a 1st 3' primer, and
5'-gggttcgagtcgctgtgtccagacagcagatgactgagaccggnnnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCGCCGAGCTCGAATCTGCGAAGCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13-14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database
of Physcomitrella EST clones is available at the PHYSCOBASE
(<http://moss.nibb.ac.jp/>).

FEATURES source

1..688
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pph26120"
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ORIGIN

Alignment Scores:
Pred. No.: 3.37e-66 Length: 688
Score: 634.00 Matches: 124
Percent Similarity: 73.04% Conservative: 25
Best Local Similarity: 60.78% Mismatches: 53
Query Match: 24.43% Indels: 2
DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJ170744 (1-688)

QY 279 SerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGln 298

446 CysLysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaVal 465
 Db TGTAGAAACACGCTCTGGTGTACGAGACGTAATCTATGTCACGGCAGCTGCAGGTT 190
 QY ValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeuHisAla 482
 Db TTGAAGCATTGAAGGAAGTCSG---GAGGCTGGCGAGCAGCATGCT 142

RESULT 5
 BJ599570/c
 LOCUS BJ599570 697 bp mRNA linear EST 22-OCT-2003
 DEFINITION BJ599570 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone ppbn26k05 3', mRNA sequence.
 ACCESSION BJ599570.1 GI:37841562
 VERSION BJ599570
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 697)
 Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 22709184
 12808149
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a l-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'- GAGAGAGAGATCCACCCCTGGAGATTTTTTTTTTTTNN-3' was used as a 1st 3' primer, and 5'-ggTTCGgTCACTCGTTCAGACGATGACTCGAGACCGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence. AGCCAAATCGCCGAGCTCGAATGTGCGAGAACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center. (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).
 Location/Qualifiers
 1. 697
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
 /sub_species="patens"
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 /clone="ppbn26k05"
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 /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
 Alignment Scores: 5.93e-60 Length: 697
 Pred. No.:

Score: 583.03 Matches: 113
 Percent Similarity: 72.19% Conservative: 22
 Best Local Similarity: 60.43% Mismatches: 50
 Query Match: 22.47% Indels: 2
 DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJ599570 (1-697)
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 QY 316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleLys 335
 Db TGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTGCGACAGGTGTGGAGAG 577
 QY 336 GlyThrValAlaPheHisTyrAlaTyrPheSerTyrAlaAlaPheHisIleLeuProGly 355
 Db GGAATGTTCTGTTTCACTACTTTGGTTCGTCGGGACAGCGGTCTCTCTCTCTCT 517
 QY 356 ValAlaLysProLeuAlaTyrMetValAlaThrGluLeuValAlaGlyLeuLeuGly 375
 Db TGGAGCCATTAGTATGATGGCGGTGACTGAGCTCATCTCCGGCATGCTGCTGGGC 460
 QY 376 PheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheVal 395
 Db TTGTATTGTACTTAGCCACATGGAGGTTTATATTCGTCTAAAGAAATTCGTG 400
 QY 396 ArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTyrPheAsnAspTyrPheThr 415
 Db AGTGCACAGATCGTATCCACCGGATATCAAGAAACATATTCAACGACTGGTTCAC 340
 QY 416 GlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsnTyr 435
 Db GGTGGCCTTAACAGGCAATAGAGCATCATCTTTTCCCAACAATGCCAGGCATATTTA 280
 QY 436 ProlLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsn 455
 Db AACAAATAGACACCTAGAGTGGAGGTGTTCTGTAAAGAACACGGTCTGGTGTACGAGAC 220
 QY 456 ValSerValValGlyAlaSerValAlaValLysAlaLeuLysGluIleAlaAspGlu 475
 Db GTAATCTATGTCACCGCAGCTTGCAGGTTTGAAGCATTTGAAGCATTTGAAGTCCGG---GAG 163
 QY 476 AlaSerIleArgLeuHisAla 482
 Db GCTGGCGCAGACGACATGCT 142

RESULT 6
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 LOCUS BJ604593 698 bp mRNA linear EST 22-OCT-2003
 DEFINITION BJ604593 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone ppbn31g10 3', mRNA sequence.
 ACCESSION BJ604593.1 GI:37846585
 VERSION BJ604593
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 698)
 Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 22709184
 12808149
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel.: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBlueScript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5' - GAAGAGAGAGAGATCCACCTGGAGAGTGTGTTTTTTTTTTTNN-3' was used as a 1st 3' primer, and 5' - ggttctcgagtcagtcgtgttccagacgcatgactcgagAACGnnnnn-3' as 2nd 5' -hairpin primer, giving the following 5' boarder sequence, AGGCATATGCGCGAGCTCGAATTCGTCGAGAACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. [2003].

Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCoBase (<http://moss.tribb.ac.jp>).

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FEATURES
  source
    Location/Qualifiers
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        /tissue_type="mixture of chloronemata, caulonemata and
        rhizoid-like protonemata"
        /clone_lib="normalized full length cDNA library,
        chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Alignment Scores:
Pred. No.:      5.95e-60      Length:      696
Score:          583.00      Matches:      113
Percent Similarity: 72.19%      Conservative: 22
Best Local Similarity: 60.43%      Mismatches:   50
Query Match:     22.47%      Indels:       2
DB:              12      Gaps:         2

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Qy	436	ProlysileAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyRAspAsn	A	455
Dd	279	AACAAANTAGCCTTAGAGTGAGGTGTTCTGTGAAGAACACCGTCTCGGTGTCAGAAGAC	A	220
Qy	456	valserValvalGlyAlaSerValAlaValvalVallysalaleuylsGluIleAlaAspGlu	A	475
Dd	219	GTAATATTGCTACCAGCACCTTCCAAGGTTTTGAAAGCATTTGAAGAGTCGG---GAG	A	163
Qy	476	AlaserIleArgLeuHisAla	A	482
Dd	162	GCTGGCGCAGCAGCATGCT	A	142
RESULT 7				
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LOCUS	Zea mays	PC0087385 mRNA sequence.	1764 bp	mRNA linear HTC 16-OCT-2002
DEFINITION				
ACCESSION	AY103762			
VERSION	AY103762.1	GI:2106840		
KEYWORDS	HTC.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD			
TITLE	Glade; Panicoideae; Andropogoneae; Zea.			
JOURNAL	1 (bases 1 to 1764)			
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,			
TITLE	Arthur,L.W., Hanafey,M., Morgante,M. and Tinsley,S.V.			
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of			
AUTHORS	Unpublished (2002)			
TITLE	2 (bases 1 to 1764)			
JOURNAL	Coe,E.H.			
AUTHORS	Direct Submission			
TITLE	Submitted (25-APR-2002) Maize Mapping Project, University of			
JOURNAL	Missouri, Columbia, MO 65211, USA			
COMMENT	If you are interested in getting corresponding physical clones,			
	these are publicly available from ZmDB and may be found by BLAST			
	searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,			
	www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the			
	maize cDNA sequences is either Virginia Walbot, Stanford or Pat			
	Schnable, Iowa State, then clones may be requested from ZmDB:			
	www.zmdb.iastate.edu.			
FEATURES	Location/Qualifiers			
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	/notes="this sequence is part of a project of EST			
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	assembled by DuPont as part of a collaboration for the			
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	Mapping Project"			
ORIGIN				
Alignment Scores:				
Pred. No.:	2,27e-57	Length:	1764	
Score:	567.50	Matches:	149	
Percent Similarity:	47.17%	Conservative:	76	
Best Local Similarity:	31.24%	Mismatches:	200	
Query Match:	21.87%	Indels:	53	
DB:	11	Gaps:	12	
US-09-980-468-2	(1-483) x AY103762	(1-1764)		
Qy	31	ProThrLeuYstHisAlaLysValSerAlaGlnGlyLysThrAlaGlyInThrLeu	A	50
Dd	45	CCAAATCAGCACCAACGAGCGGCGATCCGAGC-----ACGCCGCGCAA---TGC	A	92

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 These sequences were made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
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 DB: 29 Gaps: 18

US-09-980-468-2 (1-483) x AY418548 (1-1335)

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 Db 58 ACCTTCAGCTGGGAGGAGATTGAGAGCAATAACCTGCCACCGACAGGTGGCTGCTATT 117
 QY 82 LysGluLysValTyrAspIleSerArgPheAlaAspHisProGlyGly---ThrVal 100
 Db 118 GACCGCAAGGTTTACAACTACCAATGTTGCTCATTCAGCACCGGGGGCCGACGGGTC 177
 QY 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProProAla 120
 Db 178 ATCGGCACTACCTGGAGAGATGCAACGAGATGCTTCGCGCTTCACCCCTGACCTG 237
 QY 121 AlaTyr-----LysGlnLeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluPro 138
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 QY 139 LeuAspGlu-----LeuLeuLysAspTyrArgAspMetArgAlaGlu 152
 Db 298 AGCCAGACACGGCAGAACTCAAGATCTCTGAGGACTTCGGGCCCTTGAGAAAGACG 357
 QY 153 PheValArgGluGlyLeuPheLysSerSerLysAlaThrPheLeuLeuGlnThrLeuIle 172
 Db 358 GCTGAGGACATGAACCTGTTCAAGACCAACCAACCGTGTCTTCCTCTCTCTGGCCAC 417
 QY 173 AsnAlaLeuPheAlaSerIleAlaThrIleCysTyrAspLysSerTyrTyr--- 191
 Db 418 ATCATCGCCCTGGAGAGCACTGATGTTCACTGTTCTTTTACTTTGGCAATGGCTGAT 477
 QY 192 AlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTyrLeuAla 211
 Db 478 CCTACCTCTATCAGCGCTTTGCTTGCTGCTACCTCTCAGGCCCAAGCTGGATGGCTCAA 537
 QY 212 HisAspPheLeuHisGlnGlnValPheGlu-----AsnArgThrAlaAsnSer 227
 Db 538 CATGATTATGGCCACCTCTCTGCTACAGAAACCAAGTGAACCACTTGTGCCAAA 597
 QY 228 Phe---PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTyrTyrArg 246
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 QY 247 ThrLysHisAsnIleHisThrAlaProAsnGluCysAspGlnGlnTyrThrProLeu 266

Db 643 CATGCCACTTCAGCACACGACCAAGCCTAACATCTTCCACAAG----- 637
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 QY 284 AlaThrValGlu---SerLysArgIleLeuArgValLeuGlnTyrGlnHis--- 299
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 QY 300 -----TyrMetIleLeuProLeuPheMetAlaArgTyrSerTyrThrPheGlySer 317
 Db 793 TACTTCTCTCTGATTTGGCGCGCTGCTCTCATCCCATGAT----- 834
 QY 318 LeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThr 337
 Db 835 -----TTCCAGTACCAGATCATCATGACCATG---ATCGTCCATAAGAACTGG 879
 QY 338 ValAlaPheHisTyrAlaThrPheSerTyrAlaAlaPheHisIle-----LeuPro--- 354
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 QY 355 ---GlyValAlaLysProLeuAlaThrMetValAlaThrGluLeuValAlaGlyLeuLeu 373
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 QY 453 TyrAspAsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGlu 471
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RESULT 11
 AK083959 3318 bp mRNA linear HTC 20-SEP-2003
 LOCUS Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
 DEFINITION enriched library, clone:DL30069P05 product:DELTA-5 DESATURASE, full
 insert sequence.
 ACCESSION AK083959
 VERSION AK083959.1 GI:26350884
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCE Carninci, P. and Hayashizaki, Y.
 AUTHORS Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 2049374
 2
 REFERENCE Carninci, P. and Hayashizaki, Y.
 AUTHORS Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 2049374

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11042159
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PUBMED
REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitesunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,I., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Chara,E., Matsuura,M.,
Okada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipipillary sequencer
Genome Res. 10 (11), 1757-1771 (2000);
20530913
11076861
4
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001);
5
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3318)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Kiyashida,K., Hayatsu,M., Hiramoto,K., Hiracka,T., Hirozane,T.,
Hori,F., Imotan,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawa,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,K., Takahashi,F., Takai-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toyota,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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polyA_signal

polyA_site

ORIGIN

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Score:	527.50	Matches:	142
Percent Similarity:	45.79%	Conservative:	70
Best Local Similarity:	30.67%	Mismatches:	166
Query Match:	20.33%	Indels:	85
DB:	11	Gaps:	15

US-09-980-468-2 (1-483) x AK083959 (1-3318)

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Qy 93 AspAspHisProGlyGlyThr---ValIleSerThrTyrPheGlyArgAspGlyThrAsp 111

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Qy 184 Ile---CysTyrAspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeu 202

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SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE			
AUTHORS			
TITLE		Carninci, P. and Hayashizaki, Y.	
JOURNAL		High-efficiency full-length cDNA cloning	
MEDLINE		Meth. Enzymol. 303, 19-44 (1993);	
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REFERENCE			
AUTHORS			
TITLE		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
JOURNAL		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
MEDLINE		Genome Res. 10 (10), 1617-1630 (2000)	
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TITLE		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
JOURNAL		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer	
MEDLINE		Genome Res. 10 (11), 1757-1771 (2000)	
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AUTHORS			
TITLE		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
JOURNAL		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
MEDLINE		Nature 420, 563-573 (2002)	
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TITLE		Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,	
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 DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832423A09 product:fatty acid desaturase 3, full insert sequence.
 ACCESSION AK029318 GI:26325277
 VERSION AK029318.1
 KEYWORDS HTC; CRP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 99279253
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 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, M., Izawa, M., Okara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Kori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Tue Jun 22 14:00:29 2004

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